



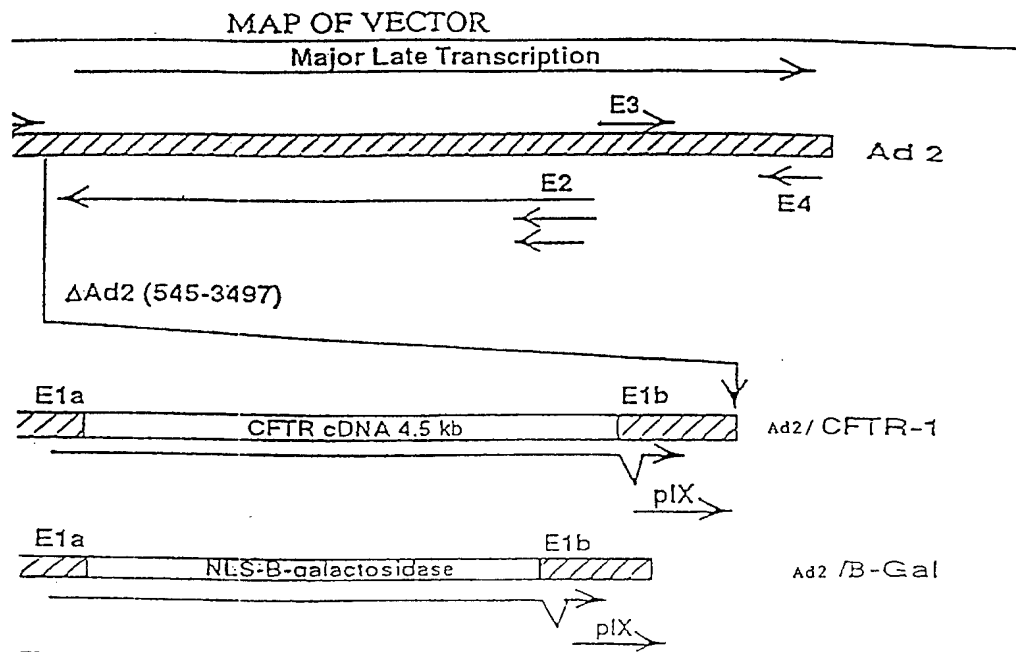
INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁵ : C12N 15/86, 15/12, A61K 48/00		A2	(11) International Publication Number: WO 94/12649
			(43) International Publication Date: 9 June 1994 (09.06.94)
(21) International Application Number: PCT/US93/11667		(81) Designated States: AU, CA, JP, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE).	
(22) International Filing Date: 2 December 1993 (02.12.93)			
(30) Priority Data: 07/985,478 3 December 1992 (03.12.92) US 08/130,682 1 October 1993 (01.10.93) US 08/136,742 13 October 1993 (13.10.93) US		Published Without international search report and to be republished upon receipt of that report.	
(71) Applicant: GENZYME CORPORATION [US/US]; One Kendall Square, Cambridge, MA 02139 (US).			
(72) Inventors: GREGORY, Richard, J.; 4789 Gateshead Road, Carlsbad, CA 92008 (US). ARMENTANO, Donna; 33 Carver Road, Watertown, MA 02172 (US). COUTURE, Larry, A.; 67 Circle Drive, Framingham, MA 01701 (US). SMITH, Alan, E.; 88 Cleveland Road, Wellesley, MA 02181 (US).			
(74) Agents: HANLEY, Elizabeth, A. et al.; Lahive & Cockfield, 60 State Street, Boston, MA 02109 (US).			

(54) Title: GENE THERAPY FOR CYSTIC FIBROSIS

(57) Abstract

Gene Therapy vectors, which are especially useful for cystic fibrosis, and methods for using the vectors are disclosed. In preferred embodiments, the vectors are adenovirus-based. Advantages of adenovirus-based vectors for gene therapy are that they appear to be relatively safe and can be manipulated to encode the desired gene product and at the same time are inactivated in terms of their ability to replicate in a normal lytic viral life cycle. Additionally, adenovirus has a natural tropism for airway epithelia. Therefore, adenovirus-based vectors are particularly preferred for respiratory gene therapy applications such as gene therapy for cystic fibrosis. In one embodiment, the adenovirus-based gene therapy vector comprises an adenovirus 2 serotype genome in which the E1a and E1b regions of the genome, which are involved in early stages of viral replication have been deleted and replaced by genetic material of interest (e.g., DNA encoding the cystic fibrosis transmembrane regulator protein). In another embodiment, the adenovirus-based therapy vector is a pseudo-adenovirus (PAV). PAVs contain no potentially harmful viral genes, have a theoretical capacity for foreign material of nearly 36 kb, may be produced in reasonably high titers and maintain the tropism of the parent adenovirus for dividing and non-dividing human target cell types.



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GENE THERAPY FOR CYSTIC FIBROSIS

Related Applications

This application is a continuation-in-part application of United States Serial Number 08/130,682, filed on October 1, 1993 which is a continuation-in-part application of United States Serial Number 07/985,478, filed on December 2, 1992, which is a continuation-in-part application of United States Serial Number 07/613,592, filed on November 15, 1990, which is in turn a continuation-in-part application of United States Serial Number 07/589,295, filed on September 27, 1990, which is itself a continuation-in-part application of United States Serial Number 07/488,307, filed on March 5, 1990. The contents of all of the above co-pending patent applications are incorporated herein by reference. Definitions of language or terms not provided in the present application are the same as those set forth in the copending applications. Any reagents or materials used in the examples of the present application whose source is not expressly identified also is the same as those described in the copending application, e.g., Δ F508 CFTR gene and CFTR antibodies.

Background of the Invention

Cystic Fibrosis (CF) is the most common fatal genetic disease in humans (Boat, T.F. et al. in *The Metabolic Basis of Inherited Diseases* (Scriver, C.R. et al. eds., McGraw-Hill, New York (1989)). Approximately one in every 2,500 infants in the United States is born with the disease. At the present time, there are approximately 30,000 CF patients in the United States. Despite current standard therapy, the median age of survival is only 26 years. Disease of the pulmonary airways is the major cause of morbidity and is responsible for 95% of the mortality. The first manifestation of lung disease is often a cough, followed by progressive dyspnea. Tenacious sputum becomes purulent because of colonization of Staphylococcus and then with Pseudomonas. Chronic bronchitis and bronchiectasis can be partially treated with current therapy, but the course is punctuated by increasingly frequent exacerbations of the pulmonary disease. As the disease progresses, the patient's activity is progressively limited. End-stage lung disease is heralded by increasing hypoxemia, pulmonary hypertension, and cor pulmonale.

The upper airways of the nose and sinuses are also involved in CF. Most patients with CF develop chronic sinusitis. Nasal polyps occur in 15-20% of patients and are common by the second decade of life. Gastrointestinal problems are also frequent in CF; infants may suffer meconium ileus. Exocrine pancreatic insufficiency, which produces symptoms of malabsorption, is present in the large majority of patients with CF. Males are almost uniformly infertile and fertility is decreased in females.

Based on both genetic and molecular analyses, a gene associated with CF was isolated as part of 21 individual cDNA clones and its protein product predicted (Kerem, B.S. et al. (1989) *Science* 245:1073-1080; Riordan, J.R. et al. (1989) *Science* 245:1066-1073;

Rommens, J.M. et al. (1989) *Science* 245:1059-1065)). United States Serial Number 07/488,307 describes the construction of the gene into a continuous strand, expression of the gene as a functional protein and confirmation that mutations of the gene are responsible for CF. (See also Gregory, R.J. et al. (1990) *Nature* 347:382-386; Rich, D.P. et al. (1990) *Nature* 347:358-362). The co-pending patent application also discloses experiments which show that proteins expressed from wild type but not a mutant version of the cDNA complemented the defect in the cAMP regulated chloride channel shown previously to be characteristic of CF.

The protein product of the CF associated gene is called the cystic fibrosis transmembrane conductance regulator (CFTR) (Riordan, J.R. et al. (1989) *Science* 245:1066-1073). CFTR is a protein of approximately 1480 amino acids made up of two repeated elements, each comprising six transmembrane segments and a nucleotide binding domain. The two repeats are separated by a large, polar, so-called R-domain containing multiple potential phosphorylation sites. Based on its predicted domain structure, CFTR is a member of a class of related proteins which includes the multi-drug resistance (MDR) or P-glycoprotein, bovine adenyl cyclase, the yeast STE6 protein as well as several bacterial amino acid transport proteins (Riordan, J.R. et al. (1989) *Science* 245:1066-1073; Hyde, S.C. et al. (1990) *Nature* 346:362-365). Proteins in this group, characteristically, are involved in pumping molecules into or out of cells.

CFTR has been postulated to regulate the outward flow of anions from epithelial cells in response to phosphorylation by cyclic AMP-dependent protein kinase or protein kinase C (Riordan, J.R. et al. (1989) *Science* 245:1066-1073; Welsh, 1986; Frizzell, R.A. et al. (1986) *Science* 233:558-560; Welsh, M.J. and Liedtke, C.M. (1986) *Nature* 322:467; Li, M. et al. (1988) *Nature* 331:358-360; Huang, T-C. et al. (1989) *Science* 244:1351-1353).

Sequence analysis of the CFTR gene of CF chromosomes has revealed a variety of mutations (Cutting, G.R. et al. (1990) *Nature* 346:366-369; Dean, M. et al. (1990) *Cell* 61:863-870; and Kerem, B-S. et al. (1989) *Science* 245:1073-1080; Kerem, B-S. et al. (1990) *Proc. Natl. Acad. Sci. USA* 87:8447-8451). Population studies have indicated that the most common CF mutation, a deletion of the 3 nucleotides that encode phenylalanine at position 508 of the CFTR amino acid sequence ($\Delta F508$), is associated with approximately 70% of the cases of cystic fibrosis. This mutation results in the failure of an epithelial cell chloride channel to respond to cAMP (Frizzell R.A. et al. (1986) *Science* 233:558-560; Welsh, M.J. (1986) *Science* 232:1648-1650.; Li, M. et al. (1988) *Nature* 331:358-360; Quinton, P.M. (1989) *Clin. Chem.* 35:726-730). In airway cells, this leads to an imbalance in ion and fluid transport. It is widely believed that this causes abnormal mucus secretion, and ultimately results in pulmonary infection and epithelial cell damage.

Studies on the biosynthesis (Cheng, S.H. et al. (1990) *Cell* 63:827-834; Gregory, R.J. et al. (1991) *Mol. Cell Biol.* 11:3886-3893) and localization (Denning, G.M. et al. (1992) *J. Cell Biol.* 118:551-559) of CFTR $\Delta F508$, as well as other CFTR mutants, indicate that many CFTR mutant proteins are not processed correctly and, as a result, are not delivered to the

plasma membrane (Gregory, R.J. et al. (1991) *Mol. Cell Biol.* 11:3886-3893). These conclusions are consistent with earlier functional studies which failed to detect cAMP-stimulated Cl⁻ channels in cells expressing CFTR Δ F508 (Rich, D.P. et al. (1990) *Nature* 347:358-363; Anderson, M.P. et al. (1991) *Science* 251:679-682).

5 To date, the primary objectives of treatment for CF have been to control infection, promote mucus clearance, and improve nutrition (Boat, T.F. et al. in *The Metabolic Basis of Inherited Diseases* (Scriver, C.R. et al. eds., McGraw-Hill, New York (1989)). Intensive antibiotic use and a program of postural drainage with chest percussion are the mainstays of therapy. However, as the disease progresses, frequent hospitalizations are required.

10 Nutritional regimens include pancreatic enzymes and fat-soluble vitamins. Bronchodilators are used at times. Corticosteroids have been used to reduce inflammation, but they may produce significant adverse effects and their benefits are not certain. In extreme cases, lung transplantation is sometimes attempted (Marshall, S. et al. (1990) *Chest* 98:1488).

Most efforts to develop new therapies for CF have focused on the pulmonary

15 complications. Because CF mucus consists of a high concentration of DNA, derived from lysed neutrophils, one approach has been to develop recombinant human DNase (Shak, S. et al. (1990) *Proc. Natl. Sci. Acad USA* 87:9188). Preliminary reports suggest that aerosolized enzyme may be effective in reducing the viscosity of mucus. This could be helpful in clearing the airways of obstruction and perhaps in reducing infections. In an attempt to limit

20 damage caused by an excess of neutrophil derived elastase, protease inhibitors have been tested. For example, alpha-1-antitrypsin purified from human plasma has been aerosolized to deliver enzyme activity to lungs of CF patients (McElvaney, N. et al. (1991) *The Lancet* 337:392). Another approach would be the use of agents to inhibit the action of oxidants derived from neutrophils. Although biochemical parameters have been successfully

25 measured, the long term beneficial effects of these treatments have not been established.

Using a different rationale, other investigators have attempted to use pharmacological agents to reverse the abnormally decreased chloride secretion and increased sodium absorption in CF airways. Defective electrolyte transport by airway epithelia is thought to alter the composition of the respiratory secretions and mucus (Boat, T.F. et al. in *The*

30 *Metabolic Basis of Inherited Diseases* (Scriver, C.R. et al. eds., McGraw-Hill, New York (1989); Quinton, P.M. (1990) *FASEB J.* 4:2709-2717). Hence, pharmacological treatments aimed at correcting the abnormalities in electrolyte transport could be beneficial. Trials are in progress with aerosolized versions of the drug amiloride; amiloride is a diuretic that inhibits sodium channels, thereby inhibiting sodium absorption. Initial results indicate that the drug

35 is safe and suggest a slight change in the rate of disease progression, as measured by lung function tests (Knowles, M. et al. (1990) *N. Eng. J. Med.* 322: 1189-1194; App, E. (1990) *Am. Rev. Respir. Dis.* 141:605). Nucleotides, such as ATP or UTP, stimulate purinergic receptors in the airway epithelium. As a result, they open a class of chloride channel that is different from CFTR chloride channels. *In vitro* studies indicate that ATP and UTP can stimulate

chloride secretion (Knowles, M. et al. (1991) *N. Eng. J. Med.* 325:533). Preliminary trials to test the ability of nucleotides to stimulate secretion *in vivo*, and thereby correct the electrolyte transport abnormalities are underway.

5 Despite progress in therapy, cystic fibrosis remains a lethal disease, and no current therapy treats the basic defect. However, two general approaches may prove feasible. These are: 1) protein replacement therapy to deliver the wild type protein to patients to augment their defective protein, and; 2) gene replacement therapy to deliver wild type copies of the CF associated gene. Since the most life threatening manifestations of CF involve pulmonary complications, epithelial cells of the upper airways are appropriate target cells for therapy.

10 The feasibility of gene therapy has been established by introducing a wild type cDNA into epithelial cells from a CF patient and demonstrating complementation of the hallmark defect in chloride ion transport (Rich, D.P. et al. (1990) *Nature* 347:358-363). This initial work involved cells in tissue culture, however, subsequent work has shown that to deliver the gene to the airways of whole animals, defective adenoviruses may be useful (Rosenfeld, 15 (1992) *Cell* 68:143-155). However, the safety and effectiveness of using defective adenoviruses remain to be demonstrated.

Summary of the Invention

20 In general, the instant invention relates to vectors for transferring selected genetic material of interest (e.g., DNA or RNA) to cells *in vivo*. In preferred embodiments, the vectors are adenovirus-based. Advantages of adenovirus-based vectors for gene therapy are that they appear to be relatively safe and can be manipulated to encode the desired gene product and at the same time are inactivated in terms of their ability to replicate in a normal lytic viral life cycle. Additionally, adenovirus has a natural tropism for airway epithelia. 25 Therefore, adenovirus-based vectors are particularly preferred for respiratory gene therapy applications such as gene therapy for cystic fibrosis.

In one embodiment, the adenovirus-based gene therapy vector comprises an adenovirus 2 serotype genome in which the Ela and Elb regions of the genome, which are involved in early stages of viral replication have been deleted and replaced by genetic 30 material of interest (e.g., DNA encoding the cystic fibrosis transmembrane regulator protein).

In another embodiment, the adenovirus-based therapy vector is a pseudo-adenovirus (PAV). PAVs contain no potentially harmful viral genes, have a theoretical capacity for foreign material of nearly 36 kb, may be produced in reasonably high titers and maintain the tropism of the parent adenovirus for dividing and non-dividing human target cell types. 35 PAVs comprise adenovirus inverted terminal repeats and the minimal sequences of a wild-type adenovirus type 2 genome necessary for efficient replication and packaging by a helper virus and genetic material of interest. In a preferred embodiment, the PAV contains adenovirus 2 sequences.

In a further embodiment, the adenovirus-based gene therapy vector contains the open reading frame 6 (ORF6) of adenoviral early region 4 (E4) from the E4 promoter and is deleted for all other E4 open reading frames. Optionally, this vector can include deletions in the E1 and/or E3 regions. Alternatively, the adenovirus-based gene therapy vector contains the open reading frame 3 (ORF3) of adenoviral E4 from the E4 promoter and is deleted for all other E4 open reading frames. Again, optionally, this vector can include deletions in the E1 and/or E3 regions. The deletion of non-essential open reading frames of E4 increases the cloning capacity by approximately 2 kb without significantly reducing the viability of the virus in cell culture. In combination with deletions in the E1 and/or E3 regions of adenovirus vectors, the theoretical insert capacity of the resultant vectors is increased to 8-9 kb.

The invention also relates to methods of gene therapy using the disclosed vectors and genetically engineered cells produced by the method.

Brief Description of the Tables and Drawings

Further understanding of the invention may be had by reference to the tables and figures wherein:

Table I shows CFTR mutants wherein the known association with CF (Y, yes or N, no), exon localization, domain location and presence (+) or absence (-) of bands A, B, and C of mutant CFTR species is shown. TM6, indicates transmembrane domain 6; NBD nucleotide binding domain; ECD, extracellular domain and Term, termination at 21 codons past residue 1337;

Table II shows the nucleotide sequence of Ad2/CFTR-1;

Table III depicts a nucleotide analysis of Ad2-ORF6/PGK-CFTR;

The convention for naming mutants is first the amino acid normally found at the particular residue, the residue number (Riordan, T.R. et al. (1989) *Science* 245:1066-1073). and the amino acid to which the residue was converted. The single letter amino acid code is used: D, aspartic acid; F, phenylalanine; G, glycine; I, isoleucine; K, lysine; M, methionine; N, asparagine; Q, glutamine; R, arginine; S, serine; W, tryptophan. Thus G551D is a mutant in which glycine 551 is converted to aspartic acid;

Figure 1 shows alignment of CFTR partial cDNA clones used in construction of cDNA containing complete coding sequence of the CFTR, only restriction sites relevant to the DNA constructions described below are shown;

Figure 2 depicts plasmid construction of the CFTR cDNA clone pKK-CFTR1;

Figure 3 depicts plasmid construction of the CFTR cDNA clone pKK-CFTR2;

Figure 4 depicts plasmid construction of the CFTR cDNA clone pSC-CFTR2;

5

Figure 5 shows a plasmid map of the CFTR cDNA clone pSC-CFTR2;

Figure 6 shows the DNA sequence of synthetic DNAs used for insertion of an intron into the CFTR cDNA sequence, with the relevant restriction endonuclease sites and nucleotide positions noted;

10

Figures 7A and 7B depict plasmid construction of the CFTR cDNA clone pKK-CFTR3;

Figure 8 shows a plasmid map of the CFTR cDNA pKK-CFTR3 containing an intron between nucleotides 1716 and 1717;

15

Figure 9 shows treatment of CFTR with glycosidases;

Figures 10A and 10B show an analysis of CFTR expressed from COS-7 transfected cells;

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Figures 11A and 11B show pulse-chase labeling of wild type and Δ F508 mutant CFTR in COS-7 transfected cells;

25

Figures 12A-12D show immunolocalization of wild type and Δ F508 mutant CFTR; and COS-7 cells transfected with pMT-CFTR or pMT-CFTR- Δ F508;

Figure 13 shows an analysis of mutant forms of CFTR;

30

Figure 14 shows a map of the first generation adenovirus based vector encoding CFTR (Ad2/CFTR-1);

Figure 15 shows the plasmid construction of the Ad2/CFTR-1 vector;

35

Figure 16 shows an example of UV fluorescence from an agarose gel electrophoresis of products of nested RT-PCR from lung homogenates of cotton rats which received Ad2/CFTR-1. The gel demonstrates that the homogenates were positive for virally-encoded CFTR mRNA;

Figure 17 shows an example of UV fluorescence from an agarose gel electrophoresis of products of nested RT-PCR from organ homogenates of cotton rats. The gel demonstrates that all organs of the infected rats were negative for Ad2/CFTR with the exception of the small bowel;

Figures 18A and 18B show differential cell analyses of bronchoalveolar lavage specimens from control and infected rats. These data demonstrate that none of the rats treated with Ad2/CFTR-1 had a change in the total or differential white blood cell count 4, 10, and 14 days after infection (Figure 18A) and 3, 7, and 14 days after infection (Figure 18B);

Figure 19 shows hematoxylin and eosin stained sections of cotton rat tracheas from both treated and control rats sacrificed at different time points after infection with Ad2/CFTR-1. The sections demonstrate that there were no observable differences between the treated and control rats;

Figures 20A and 20B show examples of UV fluorescence from an agarose gel electrophoresis, stained with ethidium bromide, of products of RT-PCR from nasal brushings of Rhesus monkeys after application of Ad2/CFTR-1 or Ad2/ β -Gal;

Figure 21 shows lights microscopy and immunocytochemistry from monkey nasal brushings. The microscopy revealed that there was a positive reaction when nasal epithelial cells from monkeys exposed to Ad2/CFTR-1 were stained with antibodies to CFTR;

Figure 22 shows immunocytochemistry of monkey nasal turbinate biopsies. This microscopy reveals increased immunofluorescence at the apical membrane of the surface epithelium from biopsies obtained from monkeys treated with Ad2/CFTR-1 over that seen at the apical membrane of the surface epithelium from biopsies obtained from control monkeys;

Figures 23A-23D show serum antibody titers in Rhesus monkeys after three vector administrations. These graphs demonstrate that all three monkeys treated with Ad2/CFTR-1 developed antibodies against adenovirus;

Figure 24 shows hematoxylin and eosin stained sections from monkey medial turbinate biopsies. These sections demonstrate that turbinate biopsy specimens from control monkeys could not be differentiated from those from monkeys treated with Ad2/CFTR-1 when reviewed by an independent pathologist;

Figures 25A-25I show photomicrographs of human nasal mucosa immediately before, during, and after Ad2/CFTR-1 application. These photomicrographs demonstrate that inspection of the nasal mucosa showed mild to moderate erythema, edema, and exudate in patients treated with Ad2/CFTR-1 (Figures 25A-25C) and in control patients (Figures 25G-25I). These changes were probably due to local anesthesia and vasoconstriction because when an additional patient was exposed to Ad2/CFTR in a method which did not require the use of local anesthesia or vasoconstriction, there were no symptoms and the nasal mucosa appeared normal (Figures 25D-25F);

Figure 26 shows a photomicrograph of a hematoxylin and eosin stained biopsy of human nasal mucosa obtained from the third patient three days after Ad2/CFTR-1 administration. This section shows a morphology consistent with CF, i.e., a thickened basement membrane and occasional morphonuclear cells in the submucosa, but no abnormalities that could be attributed to the adenovirus vector;

Figure 27 shows transepithelial voltage (V_t) across the nasal epithelium of a normal human subject. Amiloride (μM) and terbutaline (μM) were perfused onto the mucosal surface beginning at the times indicated. Under basal conditions (V_t) was electrically negative. Perfusion of amiloride onto the mucosal surface inhibited (V_t) by blocking apical Na^+ channels;

Figures 28A and 28B show transepithelial voltage (V_t) across the nasal epithelium of normal human subjects (Figure 28A) and patients with CF (Figure 28B). Values were obtained under basal conditions, during perfusion with amiloride (μM), and during perfusion of amiloride plus terbutaline (μM) onto the mucosal surface. Data are from seven normal subjects and nine patients with CF. In patients with CF, (V_t) was more electrically negative than in normal subjects (Figure 28B). Amiloride inhibited (V_t) in CF patients, as it did in normal subjects. However, V_t failed to hyperpolarize when terbutaline was perfused onto the epithelium in the presence of amiloride. Instead, (V_t) either did not change or became less negative, a result very different from that observed in normal subjects;

Figures 29A and 29B show transepithelial voltage (V_t) across the nasal epithelium of a third patient before (Figure 29A) and after (Figure 29B) administration of approximately 25 MOI of Ad2/CFTR-1. Amiloride and terbutaline were perfused onto the mucosal surface beginning at the times indicated. Figure 29A shows an example from the third patient before treatment. Figure 29B shows that in contrast to the response before Ad2/CFTR-1 was applied, after virus replication, in the presence of amiloride, terbutaline stimulated V_t ;

Figures 30A-30F show the time of course changes in transepithelial electrical properties before and after administration of Ad2/CFTR-1. Figures 30A and 30B are from the first patient who received approximately 1 MOI; Figures 30C and 30D are from the second patient who received approximately 3 MOI; and Figures 30E and 30F are from the third patient who received approximately 25 MOI. Figures 30A, 30C, and 30E show values of basal transepithelial voltage (V_t) and Figures 30B, 30D, and 30F show the change in transepithelial voltage (ΔV_t) following perfusion of terbutaline in the presence of amiloride. Day zero indicates the day of Ad2/CFTR-1 administration. Figures 30A, 30C, and 30E show the time course of changes in basal V_t for all three patients. The decrease in basal V_t suggests that application of Ad2/CFTR-1 corrected the CF electrolyte transport defect in nasal epithelium of all three patients. Additional evidence came from an examination of the response to terbutaline. Figures 30B, 30D, and 30F show the time course of the response. These data indicate that Ad2/CFTR-1 corrected the CF defect in Cl^- transport;

Figure 31 shows the time course of changes in transepithelial electrical properties before and after administration of saline instead of Ad2/CFTR-1 to CF patients. Day zero indicates the time of mock administration. The top graph shows basal transepithelial voltage (V_t) and the bottom graph shows the change in transepithelial voltage following perfusion with terbutaline in the presence of amiloride (ΔV_t). Closed symbols are data from two patients that received local anesthetic/vasoconstriction and placement of the applicator for thirty minutes. Open symbol is data from a patient that received local anesthetic/vasoconstriction, but not placement of the applicator. Symptomatic changes and physical findings were the same as those observed in CF patients treated with a similar administration procedure and Ad2/CFTR-1;

Figure 32 shows a map of the second generation adenovirus based vector, PAV;

Figure 33 shows the plasmid construction of a second generation adenoviral vector 6 (Ad E4 ORF6);

Figure 34 is a schematic of Ad2-ORF6/PGK-CFTR which differs from Ad2/CFTR in that the latter utilized the endogenous Ela promoter, had no poly A addition signal directly downstream of CFTR and retained an intact E4 region;

Figure 35 shows short-circuit currents from human CF nasal polyp epithelial cells infected with Ad2-ORF6/PGK-CFTR at multiplicities of 0.3, 3, and 50. At the indicated times: (1) 10 μM amiloride, (2) cAMP agonists (10 μM forskolin and 100 μM IBMX, and (3) 1 mM diphenylamine-2-carboxylate were added to the mucosal solution;

Figures 36A-36D show immunocytochemistry of nasal brushings by laser scanning microscopy of the Rhesus monkey C, before infection (36A) and on 7 days (36B); 24 (36C); and 38 (36D) after the first infection with Ad2-ORF6/PGK-CFTR;

Figures 37A-37D show immunocytochemistry of nasal brushings by laser scanning microscopy of Rhesus monkey D, before infection (37A) and on days 7 (37B); 24 (37C); and 48 (37D) after the first infection with Ad2-ORF6/PGK-CFTR;

Figures 38A-38D show immunocytochemistry of nasal brushings by laser scanning microscopy of the Rhesus monkey E, before infection (38A) and on days 7 (38B); 24 (38C); and 48 (38D) after the first infection with Ad2-ORF6/PGK-CFTR;

Figures 39A-39C show summaries of the clinical signs (or lack thereof) of infection with Ad2-ORF6/PGK-CFTR;

Figures 40A-40C shows a summary of blood counts, sedimentation rate, and clinical chemistries after infection with Ad2-ORF6/PGK-CFTR for monkeys C, D, and E. There was no evidence of a systemic inflammatory response or other abnormalities of the clinical chemistries;

Figure 41 shows summaries of white blood cells counts in monkeys C, D, and E after infection with Ad2-ORF6/PGK-CFTR. These data indicate that the administration of Ad2-ORF6/PGK-CFTR caused no change in the distribution and number of inflammatory cells at any of the time points following viral administration;

Figure 42 shows histology of submucosal biopsy performed on Rhesus monkey C on day 4 after the second viral instillation of Ad2-ORF6/PGK-CFTR. Hematoxylin and eosin stain revealed no evidence of inflammation or cytopathic changes;

Figure 43 shows histology of submucosal biopsy performed on Rhesus monkey D on day 11 after the second viral instillation of Ad2-ORF6/PGK-CFTR. Hematoxylin and eosin stain revealed no evidence of inflammation or cytopathic changes;

Figure 44 shows histology of submucosal biopsy performed on Rhesus monkey E on day 18 after the second viral instillation of Ad2-ORF6/PGK-CFTR. Hematoxylin and eosin stain revealed no evidence of inflammation or cytopathic changes; and

- 10.1 -

Figures 45A-45C show antibody titers to adenovirus prior to and after the first and second administrations of Ad2-ORF6/PGK-CFTR. Prior to administration of Ad2-ORF6/PGK-

CFTR, the monkeys had received instillations of Ad2/CFTR-1. Antibody titers measured by ELISA rose within one week after the first and second administrations of Ad2-ORF6/PGK-CFTR. Serum neutralizing antibodies also rose within a week after viral administration and peaked at day 24. No anti-adenoviral antibodies were detected by ELISA or neutralizing assay in nasal washings of any of the monkeys.

Detailed Description and Best Mode

Gene Therapy

As used herein, the phrase "gene therapy" refers to the transfer of genetic material (e.g., DNA or RNA) of interest into a host to treat or prevent a genetic or acquired disease or condition. The genetic material of interest encodes a product (e.g., a protein polypeptide, peptide or functional RNA) whose production *in vivo* is desired. For example, the genetic material of interest can encode a hormone, receptor, enzyme or (poly) peptide of therapeutic value. Examples of genetic material of interest include DNA encoding: the cystic fibrosis transmembrane regulator (CFTR), Factor VIII, low density lipoprotein receptor, beta-galactosidase, alpha-galactosidase, beta-glucocerebrosidase, insulin, parathyroid hormone, and alpha-1-antitrypsin.

Although the potential for gene therapy to treat genetic diseases has been appreciated for many years, it is only recently that such approaches have become practical with the treatment of two patients with adenosine deaminase deficiency. The protocol consists of removing lymphocytes from the patients, stimulating them to grow in tissue culture, infecting them with an appropriately engineered retrovirus followed by reintroduction of the cells into the patient (Kantoff, P. et al. (1987) *J. Exp. Med.* 166:219). Initial results of treatment are very encouraging. With the approval of a number of other human gene therapy protocols for limited clinical use, and with the demonstration of the feasibility of complementing the CF defect by gene transfer, gene therapy for CF appears a very viable option.

The concept of gene replacement therapy for cystic fibrosis is very simple; a preparation of CFTR coding sequences in some suitable vector in a viral or other carrier delivered directly to the airways of CF patients. Since disease of the pulmonary airways is the major cause of morbidity and is responsible for 95% of mortality, airway epithelial cells are preferred target cells for CF gene therapy. The first generation of CF gene therapy is likely to be transient and to require repeated delivery to the airways. Eventually, however, gene therapy may offer a cure for CF when the identity of the precursor or stem cell to air epithelial cells becomes known. If DNA were incorporated into airway stem cells, all subsequent generations of such cells would make authentic CFTR from the integrated sequences and would correct the physiological defect almost irrespective of the biochemical basis of the action of CFTR.

Although simple in concept, scientific and clinical problems face approaches to gene therapy, not least of these being that CF requires an *in vivo* approach while all gene therapy treatments in humans to date have involved *ex vivo* treatment of cells taken from the patient followed by reintroduction.

- 5 One major obstacle to be overcome before gene therapy becomes a viable treatment approach for CF is the development of appropriate vectors to infect tissue manifesting the disease and deliver the therapeutic CFTR gene. Since viruses have evolved very efficient means to introduce their nucleic acid into cells, many approaches to gene therapy make use of engineered defective viruses. However, the use of viruses *in vivo* raises safety concerns.
- 10 Although potentially safer, the use of simple DNA plasmid constructs containing minimal additional DNA, on the other hand, is often very inefficient and can result in transient protein expression.

- The integration of introduced DNA into the host chromosome has advantages in that such DNA will be passed to daughter cells. In some circumstances, integrated DNA may
- 15 also lead to high or more sustained expression. However, integration often, perhaps always, requires cellular DNA replication in order to occur. This is certainly the case with the present generation of retroviruses. This limits the use of such viruses to circumstances where cell division occurs in a high proportion of cells. For cells cultured *in vitro*, this is seldom a problem, however, the cells of the airway are reported to divide only infrequently
- 20 (Kawanami, O. et al. (1979) *An. Rev. Respir. Dis.* 120:595). The use of retroviruses in CF will probably require damaging the airways (by agents such as SO₂ or O₃) to induce cell division. This may prove impracticable in CF patients.

- Even if efficient DNA integration could be achieved using viruses, the human genome contains elements involved in the regulation of cellular growth only a small fraction of which
- 25 are presently identified. By integrating adjacent to an element such as a proto-oncogene or an anti-oncogene, activation or inactivation of that element could occur leading to uncontrolled growth of the altered cell. It is considered likely that several such activation/inactivation steps are usually required in any one cell to induce uncontrolled proliferation (R.A. Weinberg (1989) *Cancer Research* 49:3713), which may reduce somewhat the potential risk. On the
- 30 other hand, insertional mutagenesis leading to tumor formation is certainly known in animals with some nondefective retroviruses (R.A. Weinberg, *supra*; Payne, G.S. et al. (1982) *Nature* 295:209), and the large numbers of potential integrations occurring during the lifetime of a patient treated repeatedly *in vivo* with retroviruses must raise concerns on the safety of such a procedure.

- 35 In addition to the potential problems associated with viral DNA integration, a number of additional safety issues arise. Many patients may have preexisting antibodies to some of the viruses that are candidates for vectors, for example, adenoviruses. In addition, repeated use of such vectors might induce an immune response. The use of defective viral vectors

may alleviate this problem somewhat, because the vectors will not lead to productive viral life cycles generating infected cells, cell lysis or large numbers of progeny viruses.

Other issues associated with the use of viruses are the possibility of recombination with related viruses naturally infecting the treated patient, complementation of the viral defects by simultaneous expression of wild type virus proteins and containment of aerosols of the engineered viruses.

Gene therapy approaches to CF will face many of the same clinical challenges at protein therapy. These include the inaccessibility of airway epithelium caused by mucus build-up and the hostile nature of the environment in CF airways which may inactivate viruses/vectors. Elements of the vector carriers may be immunogenic and introduction of the DNA may be inefficient. These problems, as with protein therapy, are exacerbated by the absence of a good animal model for the disease nor a simple clinical end point to measure the efficacy of treatment.

15 CF Gene Therapy Vectors - Possible Options

Retroviruses - Although defective retroviruses are the best characterized system and so far the only one approved for use in human gene therapy (Miller, A.D. (1990) *Blood* 76:271), the major issue in relation to CF is the requirement for dividing cells to achieve DNA integration and gene expression. Were conditions found to induce airway cell division, the *in vivo* application of retroviruses, especially if repeated over many years, would necessitate assessment of the safety aspects of insertional mutagenesis in this context.

Adeno-Associated Virus - (AAV) is a naturally occurring defective virus that requires other viruses such as adenoviruses or herpes viruses as helper viruses (Muzyczka, N. (1992) in *Current Topics in Microbiology and Immunology* 158:97). It is also one of the few viruses that may integrate its DNA into non-dividing cells, although this is not yet certain. Vectors containing as little as 300 base pairs of AAV can be packaged and can integrate, but space for exogenous DNA is limited to about 4.5 kb. CFTR DNA may be towards the upper limit of packaging. Furthermore, the packaging process itself is presently inefficient and safety issues such as immunogenicity, complementation and containment will also apply to AAV. Nevertheless, this system is sufficiently promising to warrant further study.

Plasmid DNA - Naked plasmid can be introduced into muscle cells by injection into the tissue. Expression can extend over many months but the number of positive cells is low (Wolff, J. et al. (1989) *Science* 247:1465). Cationic lipids aid introduction of DNA into some cells in culture (Felgner, P. and Ringold, G.M. (1989) *Nature* 337:387). Injection of cationic lipid plasmid DNA complexes into the circulation of mice has been shown to result in expression of the DNA in lung (Brigham, K. et al. (1989) *Am. J. Med. Sci.* 298:278).

Instillation of cationic lipid plasmid DNA into lung also leads to expression in epithelial cells but the efficiency of expression is relatively low and transient (Hazinski, T.A. et al. (1991) *Am. J. Respir., Cell Mol. Biol.* 4:206). One advantage of the use of plasmid DNA is that it can be introduced into non-replicating cells. However, the use of plasmid DNA in the CF
5 airway environment, which already contains high concentrations of endogenous DNA may be problematic.

Receptor Mediated Entry - In an effort to improve the efficiency of plasmid DNA uptake, attempts have been made to utilize receptor-mediated endocytosis as an entry
10 mechanisms and to protect DNA in complexes with polylysine (Wu, G. and Wu, C.H. (1988) *J. Biol. Chem.* 263:14621). One potential problem with this approach is that the incoming plasmid DNA enters the pathway leading from endosome to lysosome, where much incoming material is degraded. One solution to this problem is the use of transferrin DNA-polylysine complexes linked to adenovirus capsids (Curiel, D.T. et al. (1991) *Proc. Natl. Acad. Sci. USA*
15 88:8850). The latter enter efficiently but have the added advantage of naturally disrupting the endosome thereby avoiding shuttling to the lysosome. This approach has promise but at present is relatively transient and suffers from the same potential problems of immunogenicity as other adenovirus based methods.

20 Adenovirus - Defective adenoviruses at present appear to be a promising approach to CF gene therapy (Berkner, K.L. (1988) *BioTechniques* 6:616). Adenovirus can be manipulated such that it encodes and expresses the desired gene product, (e.g., CFTR), and at the same time is inactivated in terms of its ability to replicate in a normal lytic viral life cycle. In addition, adenovirus has a natural tropism for airway epithelia. The viruses are able to
25 infect quiescent cells as are found in the airways, offering a major advantage over retroviruses. Adenovirus expression is achieved without integration of the viral DNA into the host cell chromosome, thereby alleviating concerns about insertional mutagenesis. Furthermore, adenoviruses have been used as live enteric vaccines for many years with an excellent safety profile (Schwartz, A.R. et al. (1974) *Am. Rev. Respir. Dis.* 109:233-238).
30 Finally, adenovirus mediated gene transfer has been demonstrated in a number of instances including transfer of alpha-1-antitrypsin and CFTR to the lungs of cotton rats (Rosenfeld, M.A. et al. (1991) *Science* 252:431-434; Rosenfeld et al., (1992) *Cell* 68:143-155). Furthermore, extensive studies to attempt to establish adenovirus as a causative agent in human cancer were uniformly negative (Green, M. et al. (1979) *Proc. Natl. Acad. Sci. USA*
35 76:6606).

The following properties would be desirable in the design of an adenovirus vector to transfer the gene for CFTR to the airway cells of a CF patient. The vector should allow sufficient expression of the CFTR, while producing minimal viral gene expression. There should be minimal viral DNA replication and ideally no virus replication. Finally,

recombination to produce new viral sequences and complementation to allow growth of the defective virus in the patient should be minimized. A first generation adenovirus vector encoding CFTR (Ad2/CFTR), made as described in the following Example 7, achieves most of these goals and was used in the human trials described in Example 10.

5 Figure 14 shows a map of Ad2/CFTR-1. As can be seen from the figure, this first generation virus includes viral DNA derived from the common relatively benign adenovirus 2 serotype. The Ela and Elb regions of the viral genome, which are involved in early stages of viral replication have been deleted. Their removal impairs viral gene expression and viral
10 function in some non-permissive cells.

 The CFTR coding sequence is inserted into the viral genome in place of the Ela/Elb region and transcription of the CFTR sequence is driven by the endogenous Ela promoter. This is a moderately strong promoter that is functional in a variety of cells. In contrast to
15 some adenovirus vectors (Rosenfeld, M. et al. (1992) *Cell* 68:143), this adenovirus retains the E3 viral coding region. As a consequence of the inclusion of E3, the length of the adenovirus-CFTR DNA is greater than that of the wild-type adenovirus. The greater length of the recombinant viral DNA renders it more difficult to package. This means that the growth of the Ad2/CFTR virus is impaired even in permissive cells that provide the missing
20 Ela and Elb functions.

 The E3 region of the Ad2/CFTR-1 encodes a variety of proteins. One of these proteins, gp19, is believed to interact with and prevent presentation of class I proteins of the major histocompatibility complex (MHC) (Gooding, C.R. and Wold, W.S.M. (1990) *Crit. Rev. Immunol.* 10:53). This property prevents recognition of the infected cells and thus may allow viral latency. The presence of E3 sequences, therefore, has two useful attributes; first,
25 the large size of the viral DNA renders it doubly defective for replication (i.e., it lacks early functions and is packaged poorly) and second, the absence of MHC presentation could be useful in later applications of Ad2/CFTR-1 in gene therapy involving multiple administrations because it may avoid an immune response to recombinant virus containing cells.

30 Not only are there advantages associated with the presence of E3; there may be disadvantages associated with its absence. Studies of E3 deleted virus in animals have suggested that they result in a more severe pathology (Gingsberg, H.S. et al. (1989) *Proc. Natl. Acad. Sci. (USA)* 86:3823). Furthermore, E3 deleted virus, such as might be obtained by recombination of an E1 plus E3 deleted virus with wild-type virus, is reported to outgrow
35 wild-type in tissue culture (Barkner, K.L. and Sharp, P. (1983) *Nucleic Acids Research* 11:6003). By contrast, however, a recent report of an E3 replacement vector encoding hepatitis B surface antigen, suggests that when delivered as a live enteric vaccine, such a virus replicates poorly in human compared to wild-type.

The adenovirus vector (Ad2/CFTR-1) and a related virus encoding the marker β -galactosidase (Ad2/ β -gal) have been constructed and grown in human 293 cells. These cells contain the E1 region of adenovirus and constitutively express Ela and Elb, which complement the defective adenoviruses by providing the products of the genes deleted from the vector. Because the size of its genome is greater than that of wild-type virus, Ad2/CFTR is relatively difficult to produce.

The Ad2/CFTR-1 virus has been shown to encode CFTR by demonstrating the presence of the protein in 293 cells. The Ad2/ β -gal virus was shown to produce its protein in a variety of cell lines grown in tissue culture including a monkey bronchiolar cell line (4MBR-5), primary hamster tracheal epithelial cells, human HeLa, human CF PAC cells (see Example 8) and airway epithelial cells from CF patients (Rich, O. et al. (1990) *Nature* 347:358).

Ad2/CFTR-1 is constructed from adenovirus 2 (Ad2) DNA sequences. Other varieties of adenovirus (e.g., Ad3, Ad5, and Ad7) may also prove useful as gene therapy vectors. This may prove essential if immune response against a single serotype reduces the effectiveness of the therapy.

Second Generation Adenoviral Vectors

Adenoviral vectors currently in use retain most ($\geq 80\%$) of the parental viral genetic material leaving their safety untested and in doubt. Second-generation vector systems containing minimal adenoviral regulatory, packaging and replication sequences have therefore been developed.

Pseudo-Adenovirus Vectors (PAV)-PAVs contain adenovirus inverted terminal repeats and the minimal adenovirus 5' sequences required for helper virus dependent replication and packaging of the vector. These vectors contain no potentially harmful viral genes, have a theoretical capacity for foreign material of nearly 36 kb, may be produced in reasonably high titers and maintain the tropism of the parent virus for dividing and non-dividing human target cell types.

The PAV vector can be maintained as either a plasmid-borne construct or as an infectious viral particle. As a plasmid construct, PAV is composed of the minimal sequences from wild type adenovirus type 2 necessary for efficient replication and packaging of these sequences and any desired additional exogenous genetic material, by either a wild-type or defective helper virus.

Specifically, PAV contains adenovirus 2 (Ad2) sequences as shown in Figure 17, from nucleotide (nt) 0-356 forming the 5' end of the vector and the last 109 nt of Ad2 forming the 3' end of the construct. The sequences includes the Ad2 flanking inverted terminal repeats (5'ITR) and the 5' ITR adjoining sequences containing the known packaging signal and Ela enhancer. Various convenient restriction sites have been incorporated into the

fragments, allowing the insertion of promoter/gene cassettes which can be packaged in the PAV virion and used for gene transfer (e.g. for gene therapy). The construction and propagation of PAV is described in detail in the following Example 11. By not containing most native adenoviral DNA, the PAVs described herein are less likely to produce a patient immune response or to replicate in a host.

In addition, the PAV vectors can accommodate foreign DNA up to a maximum length of nearly 36 kb. The PAV vectors therefore, are especially useful for cloning larger genes (e.g., CFTR (7.5 kb)); Factor VIII (8 kb); Factor IX (9 kb)), which, traditional vectors have difficulty accommodating. In addition, PAV vectors can be used to transfer more than one gene, or more than one copy of a particular gene. For example, for gene therapy of cystic fibrosis, PAVs can be used to deliver CFTR in conjunction with other genes such as anti proteases (e.g., antiprotease alpha-1-antitrypsin) tissue inhibitor of metalloproteinase, antioxidants (e.g., superoxide dismutase), enhancers of local host defense (e.g., interferons), mucolytics (e.g., DNase); and proteins which block inflammatory cytokines.

Ad2-E4/ORF6 Adenovirus Vectors

An adenoviral construct expressing only the open reading frame 6 (ORF6) of adenoviral early region 4 (E4) from the E4 promoter and which is deleted for all other known E4 open reading frames was constructed as described in detail in Example 12. Expression of E4 open reading frame 3 is also sufficient to provide E4 functions required for DNA replication and late protein synthesis. However, it provides these functions with reduced efficiency compared to expression of ORF6, which will likely result in lower levels of virus production. Therefore expressing ORF6, rather than ORF3, appears to be a better choice for producing recombinant adenovirus vectors.

The E4 region of adenovirus is suspected to have a role in viral DNA replication, late mRNA synthesis and host protein synthesis shut off, as well as in viral assembly (Falgout, B. and G. Ketner (1987) *J. Virol.* 61:3759-3768). Adenovirus early region 4 is required for efficient virus particle assembly. Adenovirus early region 4 encodes functions required for efficient DNA replication, late gene expression, and host cell shutoff. Halbert, D.N. et al. (1985) *J. Virol.* 56:250-257.

The deletion of non-essential open reading frames of E4 increases the cloning capacity of recombinant adenovirus vectors by approximately 2 kb of insert DNA without significantly reducing the viability of the virus in cell culture. When placed in combination with deletions in the E1 and/or E3 regions of adenovirus vectors, the theoretical insert capacity of the resultant vectors is increased to 8-9 kb. An example of where this increased cloning capacity may prove useful is in the development of a gene therapy vector encoding CFTR. As described above, the first generation adenoviral vector approaches the maximum packaging capacity for viral DNA encapsidation. As a result, this virus grows poorly and may occasionally give rise to defective progeny. Including an E4 deletion in the adenovirus

vector should alleviate these problems. In addition, it allows flexibility in the choice of promoters to drive CFTR expression from the virus. For example, strong promoters such as the adenovirus major late promoter, the cytomegalovirus immediate early promoter or a cellular promoter such as the CFTR promoter, which may be too large for first-generation
5 adenovirus can be used to drive expression.

In addition, by expressing only ORF6 of E4, these second generation adenoviral vectors may be safer for use in gene therapy. Although ORF6 expression is sufficient for viral DNA replication and late protein synthesis in immortalized cells, it has been suggested that ORF6/7 of E4 may also be required in non-dividing primary cells (Hemstrom, C. et al.
10 (1991) *J. Virol.* 65:1440-1449). The 19 kD protein produced from open reading frame 6 and 7 (ORF6/7) complexes with and activates cellular transcription factor E2F, which is required for maximal activation of early region 2. Early region 2 encodes proteins required for viral DNA replication. Activated transcription factor E2F is present in proliferating cells and is involved in the expression of genes required for cell proliferation (e.g., DHFR, c-myc),
15 whereas activated E2F is present in lower levels in non-proliferating cells. Therefore, the expression of only ORF6 of E4 should allow the virus to replicate normally in tissue culture cells (e.g., 293 cells), but the absence of ORF6/7 would prevent the potential activation of transcription factor E2F in non-dividing primary cells and thereby reduce the potential for viral DNA replication.

20

Target Tissue

Because 95% of CF patients die of lung disease, the lung is a preferred target for gene therapy. The hallmark abnormality of the disease is defective electrolyte transport by the epithelial cells that line the airways. Numerous investigators (reviewed in Quinton, F. (1990)
25 *FASEB J.* 4:2709) have observed: a) a complete loss of cAMP-mediated transepithelial chloride secretion, and b) a two to three fold increase in the rate of Na⁺ absorption. cAMP-stimulated chloride secretion requires a chloride channel in the apical membrane (Welsh, M.J. (1987) *Physiol Rev.* 67:1143-1184). The discovery that CFTR is a phosphorylation-regulated chloride channel and that the properties of the CFTR chloride channel are the same as those
30 of the chloride channels in the apical membrane, indicate that CFTR itself mediates transepithelial chloride secretion. This conclusion was supported by studies localizing CFTR in lung tissue: CFTR is located in the apical membrane of airway epithelial cells (Denning, G.M. et al. (1992) *J. Cell Biol.* 118:551) and has been reported to be present in the submucosal glands (Taussig et al., (1973) *J. Clin. Invest.* 89:339). As a consequence of loss
35 of CFTR function, there is a loss of cAMP-regulated transepithelial chloride secretion. At this time it is uncertain how dysfunction of CFTR produces an increase in the rate of Na⁺ absorption. However, it is thought that the defective chloride secretion and increased Na⁺ absorption lead to an alteration of the respiratory tract fluid and hence, to defective mucociliary clearance, a normal pulmonary defense mechanism. As a result, clearance of

inhaled material from the lung is impaired and repeated infections ensue. Although the presumed abnormalities in respiratory tract fluid and mucociliary clearance provide a plausible explanation for the disease, a precise understanding of the pathogenesis is still lacking.

5 Correction of the genetic defect in the airway epithelial cells is likely to reverse the CF pulmonary phenotype. The identity of the specific cells in the airway epithelium that express CFTR cannot be accurately determined by immunocytochemical means, because of the low abundance of protein. However, functional studies suggest that the ciliated epithelial cells and perhaps nonciliated cells of the surface epithelium are among the main cell types
10 involved in electrolyte transport. Thus, in practical terms, the present preferred target cell for gene therapy would appear to be the mature cells that line the pulmonary airways. These are not rapidly dividing cells; rather, most of them are nonproliferating and many may be terminally differentiated. The identification of the progenitor cells in the airway is uncertain. Although CFTR may also be present in submucosal glands (Trezise, A.E. and Buchwald, M.
15 (1991) *Nature* 353:434; Englehardt, J.F. et al. (1992) *J. Clin. Invest.* 90:2598-2607), there is no data as to its function at that site; furthermore, such glands appear to be relatively inaccessible.

 The airway epithelium provides two main advantages for gene therapy. First, access to the airway epithelium can be relatively noninvasive. This is a significant advantage in the
20 development of delivery strategies and it will allow investigators to monitor the therapeutic response. Second, the epithelium forms a barrier between the airway lumen and the interstitium. Thus, application of the vector to the lumen will allow access to the target cell yet, at least to some extent, limit movement through the epithelial barrier to the interstitium and from there to the rest of the body.

25

Efficiency of Gene Delivery Required to Correct The Genetic Defect

 It is unlikely that any gene therapy protocol will correct 100% of the cells that normally express CFTR. However, several observations suggest that correction of a small
30 percent of the involved cells or expression of a fraction of the normal amount of CFTR may be of therapeutic benefit.

a. CF is an autosomal recessive disease and heterozygotes have no lung disease. Thus, 50% of wild-type CFTR would appear sufficient for normal function.

35 b. This issue was tested in mixing experiments using CF cells and recombinant CF cells expressing wild-type CFTR (Johnson, L.G. et al. (1992) *Nature Gen.* 2:21). The data obtained showed that when an epithelium is reconstituted with as few as 6-10% of corrected cells, chloride secretion is comparable to that observed with an epithelium containing 100% corrected cells. Although CFTR expression in the recombinant cells is

probably higher than in normal cells, this result suggests that *in vivo* correction of all CF airway cells may not be required.

5 c. Recent observations show that CFTR containing some CF-associated mutations retains residual chloride channel activity (Sheppard, D.N. et al. (1992) *Pediatr. Pulmon Suppl.* 8:250; Strong, T.V. et al. (1991) *N. Eng. J. Med.* 325:1630). These mutations are associated with mild lung disease. Thus, even a very low level of CFTR activity may at least partly ameliorate the electrolyte transport abnormalities.

10 d. As indicated in experiments described below in Example 8, complementation of CF epithelia, under conditions that probably would not cause expression of CFTR in every cell, restored cAMP stimulated chloride secretion.

15 e. Levels of CFTR in normal human airway epithelia are very low and are barely detectable. It has not been detected using routine biochemical techniques such as immunoprecipitation or immunoblotting and has been exceedingly difficult to detect with immunocytochemical techniques (Denning, G.M. et al. (1992) *J. Cell Biol.* 118:551). Although CFTR has been detected in some cases using laser-scanning confocal microscopy, the signal is at the limits of detection and cannot be detected above background in every case.
20 Despite that minimal levels of CFTR, this small amount is sufficient to generate substantial cAMP-stimulated chloride secretion. The reason that a very small number of CFTR chloride channels can support a large chloride secretory rate is that a large number of ions can pass through a single channel (10^6 - 10^7 ions/sec) (Hille, B. (1984) Sinauer Assoc. Inc., Sunderland, MA 420-426).

25 f. Previous studies using quantitative PCR have reported that the airway epithelial cells contain at most one to two transcripts per cell (Trapnell, B.C. et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:6565).

30 Gene therapy for CF would appear to have a wide therapeutic index. Just as partial expression may be of therapeutic value, overexpression of wild-type CFTR appears unlikely to cause significant problems. This conclusion is based on both theoretical considerations and experimental results. Because CFTR is a regulated channel, and because it has a specific function in epithelia, it is unlikely that overexpression of CFTR will lead to uncontrolled
35 chloride secretion. First, secretion would require activation of CFTR by cAMP-dependent phosphorylation. Activation of this kinase is a highly regulated process. Second, even if CFTR chloride channels open in the apical membrane, secretion will not ensue without regulation of the basolateral membrane transporters that are required for chloride to enter the cell from the interstitial space. At the basolateral membrane, the sodium-potassium-chloride

cotransporter and potassium channels serve as important regulators of transepithelial secretion (Welsh, M.J. (1987) *Physiol. Rev.* 67:1143-1184).

Human CFTR has been expressed in transgenic mice under the control of the surfactant protein C (SPC) gene promoter (Whitesett, J.A. et al. (1992) *Nature Gen.* 2:13) and the casein promoter (Ditullio, P. et al (1992) *Bio/Technology* 10:74). In those mice, CFTR was overexpressed in bronchiolar and alveolar epithelial cells and in the mammary glands, respectively. Yet despite the massive overexpression in the transgenic animals, there were no observable morphologic or functional abnormalities. In addition, expression of CFTR in the lungs of cotton rats produced no reported abnormalities (Rosenfeld, M.A. et al. (1992) *Cell* 68:143-155).

The present invention is further illustrated by the following examples which in no way should be construed as being further limiting. The contents of all cited references (including literature references, issued patents, published patent applications, and co-pending patent applications) cited throughout this application are hereby expressly incorporated by reference.

EXAMPLES

Example 1 - Generation of Full Length CFTR cDNAs

Nearly all of the commonly used DNA cloning vectors are based on plasmids containing modified pMB1 replication origins and are present at up to 500 to 700 copies per cell (Sambrook et al. *Molecular Cloning: A Laboratory Manual* (Cold Spring Harbor Laboratory Press 1989). The partial CFTR cDNA clones isolated by Riordan et al. were maintained in such a plasmid. It was postulated that an alternative theory to intrinsic clone instability to explain the apparent inability to recover clones encoding full length CFTR protein using high copy number plasmids, was that it was not possible to clone large segments of the CFTR cDNA at high gene dosage in *E. coli*. Expression of the CFTR or portions of the CFTR from regulatory sequences capable of directing transcription and/or translation in the bacterial host cell might result in inviability of the host cell due to toxicity of the transcript or of the full length CFTR protein or fragments thereof. This inadvertent gene expression could occur from either plasmid regulatory sequences or cryptic regulatory sequences within the recombinant CFTR plasmid which are capable of functioning in *E. coli*. Toxic expression of the CFTR coding sequences would be greatly compounded if a large number of copies of the CFTR cDNA were present in cells because a high copy number plasmid was used. If the product was indeed toxic as postulated, the growth of cells containing full length and correct sequence would be actively disfavored. Based upon this novel hypothesis, the following procedures were undertaken. With reference to Figure 2, partial CFTR clone T16-4.5 was cleaved with restriction enzymes Sph 1 and Pst 1 and the resulting 3.9 kb restriction fragment containing exons 11 through most of exon 24 (including

an uncharacterized 119 bp insertion reported by Riordan et al. between nucleotides 1716 and 1717), was isolated by agarose gel purification and ligated between the Sph I and Pst I sites of the pMB1 based vector pkk223-3 (Brosius and Holy, (1984) *Proc. Natl. Acad. Sci.* 81:6929). It was hoped that the pMB1 origin contained within this plasmid would allow it and plasmids constructed from it to replicate at 15-20 copies per host *E. coli* cell (Sambrook et al. Molecular Cloning: A Laboratory Manual (Cold Spring Harbor Laboratory Press 1989). The resultant plasmid clone was called pkk-4.5.

Partial CFTR clone T11 was cleaved with Eco RI and Hinc II and the 1.9 kb band encoding the first 1786 nucleotides of the CFTR cDNA plus an additional 100 bp of DNA at the 5' end was isolated by agarose gel purification. This restriction fragment was inserted between the Eco RI site and Sma I restriction site of the plasmid Bluescript Sk- (Stratagene, catalogue number 212206), such that the CFTR sequences were now flanked on the upstream (5') side by a Sal I site from the cloning vector. This clone, designated T11-R, was cleaved with Sal I and Sph I and the resultant 1.8 kb band isolated by agarose gel purification. Plasmid pkk-4.5 was cleaved with Sal I and Sph I and the large fragment was isolated by agarose gel purification. The purified T11-R fragment and pkk-4.5 fragments were ligated to construct pkk-CFTR1. pkk-CFTR1 contains exons 1 through 24 of the CFTR cDNA. It was discovered that this plasmid is stably maintained in *E. coli* cells and confers no measureably disadvantageous growth characteristics upon host cells.

pkk-CFTR1 contains, between nucleotides 1716 and 1717, the 119 bp insert DNA derived from partial cDNA clone T16-4.5 described above. In addition, subsequent sequence analysis of pkk-CFTR1 revealed unreported differences in the coding sequence between that portion of CFTR1 derived from partial cDNA clone T11 and the published CFTR cDNA sequence. These undesired differences included a 1 base-pair deletion at position 995 and a C to T transition at position 1507.

To complete construction of an intact correct CFTR coding sequence without mutations or insertions and with reference to the construction scheme shown in Figure 3, pkk-CFTR1 was cleaved with Xba I and Hpa I, and dephosphorylated with calf intestinal alkaline phosphatase. In addition, to reduce the likelihood of recovering the original clone, the small unwanted Xba I/Hpa I restriction fragment from pKK-CFTR1 was digested with Sph I. T16-1 was cleaved with Xba I and Acc I and the 1.15 kb fragment isolated by agarose gel purification. T16-4.5 was cleaved with Acc I and Hpa I and the 0.65 kb band was also isolated by agarose gel purification. The two agarose gel purified restriction fragments and the dephosphorylated pKK-CFTR1 were ligated to produce pKK-CFTR2. Alternatively, pKK-CFTR2 could have been constructed using corresponding restriction fragments from the partial CFTR cDNA clone C1-1/5. pKK-CFTR2 contains the uninterrupted CFTR protein coding sequence and conferred slow growth upon *E. coli* host cells in which it was inserted, whereas pKK-CFTR1 did not. The origin of replication of pKK-CFTR2 is derived from pMB1 and confers a plasmid copy number of 15-20 copies per host cell.

Example 2 - Improving Host Cell Viability

An additional enhancement of host cell viability was accomplished by a further reduction in the copy number of CFTR cDNA per host cell. This was achieved by transferring the CFTR cDNA into the plasmid vector, pSC-3Z. pSC-3Z was constructed using the pSC101 replication origin of the low copy number plasmid pLG338 (Stoker *et al.*, Gene 18, 335 (1982)) and the ampicillin resistance gene and polylinker of pGEM-3Z (available from Promega). pLG338 was cleaved with Sph I and Pvu II and the 2.8 kb fragment containing the replication origin isolated by agarose gel purification. pGEM-3Z was cleaved with Alw NI, the resultant restriction fragment ends treated with T4 DNA polymerase and deoxynucleotide triphosphates, cleaved with Sph I and the 1.9 kb band containing the ampicillin resistance gene and the polylinker was isolated by agarose gel purification. The pLG338 and pGEM-3Z fragments were ligated together to produce the low copy number cloning vector pSC-3Z. pSC-3Z and other plasmids containing pSC101 origins of replication are maintained at approximately five copies per cell (Sambrook *et al.*, *supra*).

With additional reference to Figure 4, pKK-CFTR2 was cleaved with Eco RV, Pst I and Sal I and then passed over a Sephacryl S400 spun column (available from Pharmacia) according to the manufacturer's procedure in order to remove the Sal I to Eco RV restriction fragment which was retained within the column. pSC-3Z was digested with Sma I and Pst I and also passed over a Sephacryl S400 spun column to remove the small Sma I/Pst I restriction fragment which was retained within the column. The column eluted fractions from the pKK-CFTR2 digest and the pSC-3Z digest were mixed and ligated to produce pSC-CFTR2. A map of this plasmid is presented in Figure 5. Host cells containing CFTR cDNAs at this and similar gene dosages grow well and have stably maintained the recombinant plasmid with the full length CFTR coding sequence. In addition, this plasmid contains a bacteriophage T7 RNA polymerase promoter adjacent to the CFTR coding sequence and is therefore convenient for *in vitro* transcription/translation of the CFTR protein. The nucleotide sequence of CFTR coding region from pSC-CFTR2 plasmid is presented in Sequence Listing 1 as SEQ ID NO:1. Significantly, this sequence differs from the previously published (Riordan, J.R. et al. (1989) *Science* 245:1066-1073) CFTR sequence at position 1990, where there is C in place of the reported A. See Gregory, R.J. et al. (1990) *Nature* 347:382-386. *E. coli* host cells containing pSC-CFTR2, internally identified with the number pSC-CFTR2/AG1, have been deposited at the American Type Culture Collection and given the accession number: ATCC 68244.

Example 3 - Alternate Method for Improving Host Cell Viability

A second method for enhancing host cell viability comprises disruption of the CFTR protein coding sequence. For this purpose, a synthetic intron was designed for insertion between nucleotides 1716 and 1717 of the CFTR cDNA. This intron is especially

advantageous because of its easily manageable size. Furthermore, it is designed to be efficiently spliced from CFTR primary RNA transcripts when expressed in eukaryotic cells. Four synthetic oligonucleotides were synthesized (1195RG, 1196RG, 1197RG and 1198RG) collectively extending from the Sph I cleavage site at position 1700 to the Hinc II cleavage site at position 1785 and including the additional 83 nucleotides between 1716 and 1717 (see Figure 6). These oligonucleotides were phosphorylated with T4 polynucleotide kinase as described by Sambrook et al., mixed together, heated to 95°C for 5 minutes in the same buffer used during phosphorylation, and allowed to cool to room temperature over several hours to allow annealing of the single stranded oligonucleotides. To insert the synthetic intron into the CFTR coding sequence and with reference to Figures 7A and 7B, a subclone of plasmid T11 was made by cleaving the Sal I site in the polylinker, repairing the recessed ends of the cleaved DNA with deoxynucleotide triphosphates and the large fragment of DNA Polymerase I and religating the DNA. This plasmid was then digested with Eco RV and Nru I and religated. The resulting plasmid T16-Δ5' extended from the Nru I site at position 490 of the CFTR cDNA to the 3' end of clone T16 and contained single sites for Sph I and Hinc II at positions corresponding to nucleotides 1700 and 1785 of the CFTR cDNA. T16-Δ5' plasmid was cleaved with Sph I and Hinc II and the large fragment was isolated by agarose gel purification. The annealed synthetic oligonucleotides were ligated into this vector fragment to generate T16-intron.

T16-intron was then digested with Eco RI and Sma I and the large fragment was isolated by agarose gel purification. T16-4.5 was digested with Eco RI and Sca I and the 790 bp fragment was also isolated by agarose gel purification. The purified T16-intron and T16-4.5 fragments were ligated to produce T16-intron-2. T16-intron-2 contains CFTR cDNA sequences extending from the Nru I site at position 490 to the Sca I site at position 2818, and includes the unique Hpa I site at position 2463 which is not present in T16-1 or T16-intron-1.

T16-intron-2 was then cleaved with Xba I and Hpa I and the 1800 bp fragment was isolated by agarose gel purification. pKK-CFTR1 was digested with Xba I and Hpa I and the large fragment was also isolated by agarose gel purification and ligated with the fragment derived from T16-intron-2 to yield pKK-CFTR3, shown in Figure 8. The CFTR cDNA within pKK-CFTR3 is identical to that within pSC-CFTR2 and pKK-CFTR2 except for the insertion of the 83 bp intron between nucleotides 1716 and 1717. The insertion of this intron resulted in improved growth characteristics for cells harboring pKK-CFTR3 relative to cells containing the unmodified CFTR cDNA in pKK-CFTR2.

Example 4 - In vitro Transcription/Translation

In addition to sequence analysis, the integrity of the CFTR cDNA open reading frame was verified by *in vitro* transcription/translation. This method also provided the initial CFTR protein for identification purposes. 5 micrograms of pSC-CFTR2 plasmid DNA were linearized with Sal I and used to direct the synthesis of CFTR RNA transcripts with T7 RNA

polymerase as described by the supplier (Stratagene). This transcript was extracted with phenol and chloroform and precipitated with ethanol. The transcript was resuspended in 25 microliters of water and varying amounts were added to a reticulocyte lysate *in vitro* translation system (Promega). The reactions were performed as described by the supplier in the presence of canine pancreatic microsomal membranes (Promega), using ³⁵S-methionine to label newly synthesized proteins. *In vitro* translation products were analysed by discontinuous polyacrylamide gel electrophoresis in the presence of 0.1% SDS with 8% separating gels (Laemmli, U.K. (1970) *Nature* 227:680-685). Before electrophoresis, the *in vitro* translation reactions were denatured with 3% SDS, 8 M urea and 5% 2-mercaptoethanol in 0.65 M Tris-HCl, pH 6.8. Following electrophoresis, the gels were fixed in methanol:acetic acid:water (30:10:60), rinsed with water and impregnated with 1 M sodium salicylate. ³⁵S labelled proteins were detected by fluorography. A band of approximately 180 kD was detected, consistent with translation of the full length CFTR insert.

15

Example 5 - Elimination of Cryptic Regulatory Signals

Analysis of the DNA sequence of the CFTR has revealed the presence of a potential *E. coli* RNA polymerase promoter between nucleotides 748 and 778 which conforms well to the derived consensus sequence for *E. coli* promoters (Reznikoff and McClure, Maximizing Gene Expression, 1, Butterworth Publishers, Stoneham, MA). If this sequence functions as a promoter functions in *E. coli*, it could direct synthesis of potentially toxic partial CFTR polypeptides. Thus, an additional advantageous procedure for maintaining plasmids containing CFTR cDNAs in *E. coli* would be to alter the sequence of this potential promoter such that it will not function in *E. coli*. This may be accomplished without altering the amino acid sequence encoded by the CFTR cDNA. Specifically, plasmids containing complete or partial CFTR cDNA's would be altered by site-directed mutagenesis using synthetic oligonucleotides (Zoller and Smith, (1983) *Methods Enzymol.* 100:468). More specifically, altering the nucleotide sequence at position 908 from a T to C and at position 774 from an A to a G effectively eliminates the activity of this promoter sequence without altering the amino acid coding potential of the CFTR open reading frame. Other potential regulatory signals within the CFTR cDNA for transcription and translation could also be advantageously altered and/or deleted by the same method.

Further analysis has identified a sequence extending from nucleotide 908 to 936 which functions efficiently as a transcriptional promoter element in *E. coli* (Gregory, R.J. et al. (1990) *Nature* 347:382-386). Mutation at position 936 is capable of inactivating this promoter and allowing the CFTR cDNA to be stably maintained as a plasmid in *E. coli* (Cheng, S.H. et al. (1990) *Cell* 63:827-834). Specifically position 936 has been altered from a C to a T residue without the amino acid sequence encoded by the cDNA being altered. Other mutations within this regulatory element described in Gregory, R.J. et al. (1990)

Nature 347:382-386 could also be used to inactivate the transcriptional promoter activity. Specifically, the sequence from 908 to 913 (TTGTGA) and from 931 to 936 (GAAAAT) could be altered by site directed mutagenesis without altering the amino acid sequence encoded by the cDNA.

5

Example 6 - Cloning of CFTR in Alternate Host Systems

Although the CFTR cDNA displays apparent toxicity in *E. coli* cells, other types of host cells may not be affected in this way. Alternative host systems in which the entire CFTR cDNA protein encoding region may be maintained and/or expressed include other
10 bacterial species and yeast. It is not possible *a priori* to predict which cells might be resistant and which might not. Screening a number of different host/vector combinations is necessary to find a suitable host tolerant of expression of the full length protein or potentially toxic fragments thereof.

15

Example 7 - Generation of Adenovirus Vector Encoding CFTR (Ad2/CFTR)

1. DNA preparation - Construction of the recombinant Ad2/CFTR-1 virus (the sequence of which is shown in Table II and as SEQ ID NO:3) was accomplished as follows: The CFTR cDNA was excised from the plasmid pCMV-CFTR-936C using restriction enzymes
20 SpeI and EcoII361. pCMV-CFTR-936C consists of a minimal CFTR cDNA encompassing nucleotides 123-4622 of the published CFTR sequence cloned into the multiple cloning site of pRC/CMV (Invitrogen Corp.) using synthetic linkers. The CFTR cDNA within this plasmid has been completely sequenced. The SpeI/EcoII361 restriction fragment contains 47 bp of 5' sequence derived from synthetic linkers and the multiple cloning site of the vector.

25

The CFTR cDNA (the sequence of which is shown as SEQ ID NO:1 and the amino acid sequence encoded by the CFTR cDNA is shown as SEQ ID NO:2) was inserted between the NheI and SnaBI restriction sites of the adenovirus gene transfer vector pBR-Ad2-7. pBR-Ad2-7 is a pBR322 based plasmid containing an approximately 7 kb insert derived from the 5' 10680 bp of Ad2 inserted between the Clal and BamHI sites of pBR322. From this Ad2
30 fragment, the sequences corresponding to Ad2 nucleotides 546-3497 were deleted and replaced with a 12 bp multiple cloning site containing an NheI site, an MluI site, and a SnaBI site. The construct also contains the 5' inverted terminal repeat and viral packaging signals, the Ela enhancer and promoter, the Elb 3' intron and the 3' untranslated region and polyadenylation sites. The resulting plasmid was called pBR-Ad2-7/CFTR. Its use to
35 assemble virus is described below.

2. Virus Preparation from DNA - To generate the recombinant Ad2/CFTR-1 adenovirus, the vector pBR-Ad2-7/CFTR was cleaved with BstBI at the site corresponding to the unique BstBI site at 10670 in Ad2. The cleaved plasmid DNA was ligated to BstBI restricted Ad2

DNA. Following ligation, the reaction was used to transfect 293 cells by the calcium phosphate procedure. Approximately 7-8 days following transfection, a single plaque appeared and was used to reinfect a dish of 293 cells. Following development of cytopathic effect (CPE), the medium was removed and saved. Total DNA was prepared from the infected cells and analyzed by restriction analysis with multiple enzymes to verify the integrity of the construct. Viral supernatant was then used to infect 293 cells and upon development of CPE, expression of CFTR was assayed by the protein kinase A (PKA) immunoprecipitation assay (Gregory, R.J. et al. (1990) *Nature* 347:382). Following these verification procedures, the virus was further purified by two rounds of plaque purification.

Plaque purified virus was grown into a small seed stock by inoculation at low multiplicities of infection onto 293 cells grown in monolayers in 925 medium supplemented with 10% bovine calf serum. Material at this stage was designated a Research Viral Seed Stock (RVSS) and was used in all preliminary experiments.

3. Virus Host Cell - Ad2/CFTR-1 is propagated in human 293 cells (ATCC CRL 1573). These cells are a human embryonal kidney cell line which were immortalized with sheared fragments of human Ad5 DNA. The 293 cell line expresses adenovirus early region 1 gene products and in consequence, will support the growth of E1 deficient adenoviruses. By analogy with retroviruses, 293 cells could be considered a packaging cell line, but they differ from usual retrovirus lines in that they do not provide missing viral structural proteins, rather, they provide only some missing viral early functions.

Production lots of virus are propagated in 293 cells derived from the Working Cell Bank (WCB). The WCB is in turn derived from the Master Cell Bank (MCB) which was grown up from a fresh vial of cells obtained from ATCC. Because 293 cells are of human origin, they are being tested extensively for the presence of biological agents. The MCB and WCB are being characterized for identity and the absence of adventitious agents by Microbiological Associates, Rockville, MD.

4. Growth of Production Lots of Virus

Production lots of Ad2/CFTR-1 are produced by inoculation of approximately $5-10 \times 10^7$ pfu of MVSS onto approximately $1-2 \times 10^7$ Wcb 293 cells grown in a T175 flask containing 25 mls of 925 medium. Inoculation is achieved by direct addition of the virus (approximately 2-5 mls) to each flask. Batches of 50-60 flasks constitute a lot.

Following 40-48 hours incubation at 37°C, the cells are shaken loose from the flask and transferred with medium to a 250 ml centrifuge bottle and spun at 1000 xg. The cell pellet is resuspended in 4 ml phosphate buffered saline containing 0.1 g/l CaCl_2 and 0.1g/l MgCl_2 and the cells subjected to cycles of freeze-thaw to release virus. Cellular debris is removed by centrifugation at 1000 xg for 15 min. The supernatant from this centrifugation is layered on top of the CsCl step gradient: 2 ml 1.4g/ml CsCl and 3 ml 1.25g/ml CsCl in 10

mM Tris, 1 mM EDTA (TE) and spun for 1 hour at 35,000 rpm in a Beckman SW41 rotor. Virus is then removed from the interface between the two CsCl layers, mixed with 1.35 g/ml CsCl in TE and then subjected to a 2.5 hour equilibrium centrifugation at 75,000 rpm in a TLN-100 rotor. Virus is removed by puncturing the side of the tube with a hypodermic
5 needle and gently removing the banded virus. To reduce the CsCl concentration, the sample is dialyzed against 2 changes of 2 liters of phosphate buffered saline with 10% sucrose.

Following this procedure, dialyzed virus is stable at 4°C for several weeks or can be stored for longer periods at -80°C. Aliquots of material for human use will be tested and while awaiting the results of these tests, the remainder will be stored frozen. The tests to be
10 performed are described below:

5. Structure and Purity of Virus

SDS polyacrylamide gel electrophoresis of purified virions reveals a number of polypeptides, many of which have been characterized. When preparations of virus were
15 subjected to one or two additional rounds of CsCl centrifugation, the protein profile obtained was indistinguishable. This indicates that additional equilibrium centrifugation does not purify the virus further, and may suggest that even the less intense bands detected in the virus preparations represent minor virion components rather than contaminating proteins. The identity of the protein bands is presently being established by N-terminal sequence analysis.

20

6. Contaminating Materials - The material to be administered to patients will be 2×10^6 pfu, 2×10^7 pfu and 5×10^7 pfu of purified Ad2/CFTR-1. Assuming a minimum particle to pfu ratio of 500, this corresponds to 1×10^9 , 1×10^{10} and 2.5×10^{10} viral particles, these correspond to a dose by mass of 0.25 µg, 2.5µg and 6.25 µg assuming a molecular mass for
25 adenovirus of 150×10^6 .

The origin of the materials from which a production lot of the purified Ad2/CFTR-1 is derived was described in detail above and is illustrated as a flow diagram in Figure 6. All the starting materials from which the purified virus is made (i.e., MCB, and WCB, and the MVSS) will be extensively tested. Further, the growth medium used will be tested and the
30 serum will be from only approved suppliers who will provide test certificates. In this way, all the components used to generate a production lot will have been characterized. Following growth, the production lot virus will be purified by two rounds of CsCl centrifugation, dialyzed, and tested. A production lot should constitute $1-5 \times 10^{10}$ pfu Ad2/CFTR-1.

As described above, to detect any contaminating material aliquots of the production
35 lot will be analyzed by SDS gel electrophoresis and restriction enzyme mapping. However, these tests have limited sensitivity. Indeed, unlike the situation for purified single chain recombinant proteins, it is very difficult to quantitate the purity of the AD2/CFTR-1 using SDS polyacrylamide gel electrophoresis (or similar methods). An alternative is the immunological detection of contaminating proteins (IDCP). Such an assay utilizes antibodies

raised against the proteins purified in a mock purification run. Development of such an assay has not yet been attempted for the CsCl purification scheme for Ad2/CFTR-1. However, initially an IDCP assay developed for the detection of contaminants in recombinant proteins produced in Chinese hamster ovary (CHO) cells will be used. In addition, to hamster
5 proteins, these assays detect bovine serum albumin (BSA), transferrin and IgG heavy and light chain derived from the serum added to the growth medium. Tests using such reagents to examine research batches of Ad2/CFTR-1 by both ELISA and Western blots are in progress.

Other proteins contaminating the virus preparation are likely to be from the 293 cells - that is, of human origin. Human proteins contaminating therapeutic agents derived from
10 human sources are usually not problematic. In this case, however, we plan to test the production lot for transforming factors. Such factors could be activities of contaminating human proteins or of the Ad2/CFTR-1 vector or other contaminating agents. For the test, it is proposed that 10 dishes of Rat 1 cells containing 2×10^6 cells (the number of target cells in the patient) with 4 times the highest human dose of Ad2/CFTR-1 (2×10^8 pfu) will be
15 infected. Following infection, the cells will be plated out in agar and examined for the appearance of transformed foci for 2 weeks. Wild type adenovirus will be used as a control.

Nucleic acids and proteins would be expected to be separated from purified virus preparations upon equilibrium density centrifugation. Furthermore, the 293 cells are not expected to contain VL30 sequences. Biologically active nucleic cells should be detected.

20

Example 8 - Preliminary Experiments Testing the Ability of Ad2/ β Gal or Ad2/CFTR Virus to Enter Airway Epithelial Cells

a. Hamster Studies

25 Initial studies involving the intratracheal instillation of the Ad- β Gal viral vector into Syrian hamsters, which are reported to be permissive for human adenovirus are being performed. The first study, a time course assessment of the pulmonary and systemic acute inflammatory response to a single intratracheal administration of Ad- β Gal viral vector, has been completed. In this study, a total of 24 animals distributed among three treatment
30 groups, specifically, 8 vehicle control, 8 low dose virus (1×10^{11} particles; 3×10^8 pfu), and 8 high dose virus (1.7×10^{12} particles; 5×10^9 pfu), were used. Within each treatment group, 2 animals were analyzed at each of four time points after viral vector instillation: 6 hrs, 24 hrs, 48 hrs, and 7 days. At the time of sacrifice of each animal, lung lavage and blood samples were taken for analysis. The lungs were fixed and processed for normal light-level
35 histology. Blood and lavage fluid were evaluated for total leukocyte count and leukocyte differential. As an additional measure of the inflammatory process, lavage fluid was also evaluated for total protein. Following embeddings, sectioning and hematoxylin/eosin staining, lung sections were evaluated for signs of inflammation and airway epithelial damage.

With the small sample size, the data from this preliminary study were not amenable to statistical analyses, however, some general trends could be ascertained. In the peripheral blood samples, total leukocyte counts showed no apparent dose- or time- dependent changes. In the blood leukocyte differential counts, there may have been a minor dose-related
5 elevation in percent neutrophil at 6 hours; however, data from all other time points showed no elevation in neutrophil percentages. Taken together, these data suggest little or nor systemic inflammatory response to the viral administration.

From the lung lavage, some elevation in total neutrophil counts were observed at the first three time points (6 hr, 24 hr, 48 hr). By seven days, both total and percent neutrophil
10 values had returned to normal range. The trends in lung lavage protein levels were more difficult to assess due to inter-animal variability; however, no obvious dose- or time- dependent effects were apparent. First, no damage to airway epithelium was observed at any time point or virus dose level. Second, a time- and dose- dependent mild inflammatory response was observed, being maximal at 48 hr in the high virus dose animals. By seven
15 days, the inflammatory response had completely resolved, such that the lungs from animals in all treatment groups were indistinguishable.

In summary, a mild, transient, pulmonary inflammatory response appears to be associated with the intratracheal administration of the described doses of adenoviral vector in the Syrian Hamster.

20 A second, single intratracheal dose, hamster study has been initiated. This study is designed to assess the possibility of the spread of ineffective viral vectors to organs outside of the lung and the antibody response of the animals to the adenoviral vector. In this study, the three treatment groups (vehicle control, low dose virus, high dose virus) each contained 12 animals. Animals will be evaluated at three time points: 1 day, 7 days, and 1 month. In this
25 study, viral vector persistence and possible spread will be evaluated by the assessment of the presence of infective virions in numerous organs including lung, gut, heart, liver, spleen, kidney, brain and gonads. Changes in adenoviral antibody titer will be measured in peripheral blood and lung lavage. Additionally, lung lavage, peripheral blood and lung histology will be evaluated as in the previous study.

30 b. Primate studies.

Studies of recombinant adenovirus are also underway in primates. The goal of these studies is to assess the ability of recombinant adenoviral vectors to deliver genes to the respiratory epithelium *in vivo* and to assess the safety of the construct in primates. Initial
35 studies in primates targeted nasal epithelia as the site of infection because of its similarity to lower airway epithelia, because of its accessibility, and because nasal epithelia was used for the first human studies. The Rhesus monkey (*Macaca mulatta*) has been chosen for studies, because it has a nasal epithelium similar to that of humans.

How expression of CFTR affects the electrolyte transport properties of the nasal epithelium can be studied in patients with cystic fibrosis. But because the primates have normal CFTR function, instead the ability to transfer a reporter gene was assessed. Therefore the Ad- β Gal virus was used. The epithelial cell density in the nasal cavity of the Rhesus monkey is estimated to be 2×10^6 cells/cm (based on an average nasal epithelial cell diameter of 7 μ m) and the surface near 25-50 cm². Thus, there are about 5×10^7 cells in the nasal epithelium of Rhesus monkey. To focus especially on safety, the higher viral doses (20-200 MOI) were used *in vivo*. Thus doses in the range of 10^9 - 10^{10} pfu were used.

In the first pilot study the right nostril of Monkey A was infected with Ad- β -Gal (~1 ml). This viral preparation was purified by CsCl gradient centrifugation and then by gel filtration chromatography one week later. Adenoviruses are typically stable in CsCl at 4°C for one to two weeks. However, this viral preparation was found to be defective (i.e., it did not produce detectable β -galactosidase activity in the permissive 293 cells). Thus, it was concluded that there was no live viral activity in the material. β -galactosidase activity in nasal epithelial cells from Monkey A was also not detected. Therefore, in the next study, two different preparations of Ad- β -Gal virus: one that was purified on a CsCl gradient and then dialyzed against Tris-buffered saline to remove the CsCl, and a crude unpurified one was used. Titers of Ad- β -Gal viruses were $\sim 2 \times 10^{10}$ pfu/ml and $> 1 \times 10^{13}$ pfu/ml, respectively, and both preparations produced detectable β -galactosidase activity in 293 cells.

Monkeys were anesthetized by intramuscular injection of ketamine (15 mg/kg). One week before administration of virus, the nasal mucosa of each monkey was brushed to establish baseline cell differentials and levels of β -galactosidase. Blood was drawn for baseline determination of cell differentials, blood chemistries, adenovirus antibody titers, and viral cultures. Each monkey was also examined for weight, temperature, appetite, and general health prior to infection.

The entire epithelium of one nasal cavity was used in each monkey. A foley catheter (size 10) was inserted through each nasal cavity into the pharynx, inflated with 2-3 ml of air, and then pulled anteriorly to obtain tight posterior occlusion at the posterior choana. Both nasal cavities were then irrigated with a solution (~5 ml) of 5 mM dithiothreitol plus 0.2 U/ml neuraminidase in phosphate-buffered saline (PBS) for five minutes. This solution was used to dissolve any residual mucus overlaying the epithelia. (It was subsequently found that such treatment is not required.) The washing procedure also allowed the determination of whether the balloons were effectively isolating the nasal cavity. The virus (Ad- β -Gal) was then slowly instilled into the right nostril with the posterior balloon inflated. The viral solution remained in contact with the nasal mucosa for 30 minutes. At the end of 30 minutes, the remaining viral solution was removed by suction. The balloons were deflated, the catheters removed, and the monkey allowed to recover from anesthesia. Monkey A received the CsCl-purified virus (~1.5 ml) and Monkey B received the crude virus (~6 ml). (note that this was the second exposure of Monkey A to the recombinant adenovirus).

Both monkeys were followed daily for appearance of the nasal mucosa, conjunctivitis, appetite, activity, and stool consistency. Each monkey was subsequently anesthetized on days 1, 4, 7, 14, and 21 to obtain nasal, pharyngeal, and tracheal cell samples (either by swabs or brushes) as described below. Phlebotomy was performed over the same time course
5 for hematology, ESR, general screen, antibody serology and viral cultures. Stools were collected every week to assess viral cultures.

To obtain nasal epithelial cells from an anesthetized monkey, the nasal mucosa was first impregnated with 5 drops of Afrin (0.05% oxymetazoline hydrochloride, Schering-Plough) and 1 ml of 2% Lidocaine for 5 min. A cytobrush (the kind typically used for Pap
10 smears) was then used to gently rub the mucosa for about 10 seconds. For tracheal brushings, a flexible fiberoptic bronchoscope; a 3 mm cytology brush (Bard) was advanced through the bronchoscope into the trachea, and a small area was brushed for about 10 seconds. This procedure was repeated twice to obtain a total of $\sim 10^6$ cells/ml. Cells were then collected on slides (approximately 2×10^4 cells/slide using a Cytospin 3 (Shandon, PA)) for subsequent
15 staining (see below).

To determine viral efficacy, nasal, pharyngeal, and tracheal cells were stained for β -galactosidase using X-gal (5 bromo-4-chloro-3-indolyl- β -D-galactoside). Cleavage of X-gal by β -galactosidase produces a blue color that can be seen with light microscopy. The Ad- β -gal vector included a nuclear-localization signal (NLS) (from SV40 large T-antigen) at the
20 amino-terminus of the β -galactosidase sequence to direct expression of this protein to the nucleus. Thus, the number of blue nuclei after staining was determined.

RT-PCR (reverse transcriptase-polymerase chain reaction) was also used to determine viral efficacy. This assay indicates the presence of β -galactosidase mRNA in cells obtained by brushings or swabs. PCR primers were used in both the adenovirus sequence and the
25 LacZ sequence to distinguish virally-produced mRNA from endogenous mRNA. PCR was also used to detect the presence of the recombinant adenovirus DNA. Cytospin preparations was used to assess for the presence of virally produced β -galactosidase mRNA in the respiratory epithelial cells using *in-situ* hybridization. This technique has the advantage of being highly specific and will allow assessment which cells are producing the mRNA.

30 Whether there was any inflammatory response was assessed by visual inspection of the nasal epithelium and by cytological examination of Wright-stained cells (cytospin). The percentage of neutrophils and lymphocytes were compared to that of the control nostril and to the normal values from four control monkeys. Systemic responses by white blood cell counts, sedimentation rate, and fever were also assessed.

35 Viral replication at each of the time points was assessed by testing for the presence of live virus in the supernatant of the cell suspension from swabs or brushes. Each supernatant was used to infect (at several dilutions) the virus-sensitive 293 cell line. Cytopathic changes in the 293 cells were monitored for 1 week and then the cells were fixed and stained for β -galactosidase. Cytopathic effects and blue-stained cells indicated the presence of live virus.

Positive supernatants will also be subjected to analysis of nonintegrating DNA to identify (confirm) the contributing virus(es).

Antibody titers to type 2 adenovirus and to the recombinant adenovirus were determined by ELISA. Blood/serum analysis was performed using an automated chemistry analyzer Hitachi 737 and an automated hematology analyzer Technicom H6. The blood buffy coat was cultured in A549 cells for wild type adenovirus and was cultured in the permissive 293 cells.

Results: Both monkeys tolerated the procedure well. Daily examination revealed no evidence of coryza, conjunctivitis or diarrhea. For both monkeys, the nasal mucosa was mildly erythematous in both the infection side and the control side; this was interpreted as being due to the instrumentation. Appetites and weights were not affected by virus administered in either monkey. Physical examination on days 1, 4, 7, 14 and 21 revealed no evidence of lymphadenopathy, tachypnea, or tachycardia. On day 21, monkey B had a temperature 39.1°C (normal for Rhesus monkey 38.8°C) but had no other abnormalities on physical exam or in laboratory data. Monkey A had a slight leukocytosis on day 1 post infection which returned to normal by day 4; the WBC was 4,920 on the day of infection, 8,070 on day 1, and 5,200 on day 4. The ESR did not change after the infection. Electrolytes and transaminases were normal throughout.

Wright stains of cells from nasal brushing were performed on days 4, 7, 14, and 21. They revealed less than 5% neutrophils and lymphocytes. There was no difference between the infected and the control side.

X-Gal stains of the pharyngeal swabs revealed blue-stained cells in both monkeys on days 4, 7, and 14; only a few of the cells had clear nuclear localization of the pigment and some pigment was seen in extracellular debris. On day 7 post infection, X-Gal stains from the right nostril of monkey A, revealed a total of 135 ciliated cells with nuclear-localized blue stain. The control side had only 4 blue cells. Monkey B had 2 blue cells from the infected nostril and none from the control side. Blue cells were not seen on day 7, 14, or 21.

RT-PCR on day 3 post infection revealed a band of the correct size that hybridized with a β -Gal probe, consistent with β -Gal mRNA in the samples from Monkey A control nostril and Monkey B infected nostril. On day 7 there was a positive band in the sample from the infected nostril of Monkey A, the same specimen that revealed blue cells.

Fluid from each nostril, the pharynx, and trachea of both monkeys was placed on 293 cells to check for the presence of live virus by cytopathic effect and X-Gal stain. In Monkey A, live virus was detected in both nostrils on day 3 after infection; no live virus was detected at either one or two weeks post-infection. In Monkey B, live virus was detected in both nostrils, pharynx, and trachea on day 3, and only in the infected nostril on day 7 after infection. No live virus was detected 2 weeks after the infection.

c. Human Explant Studies

In a second type of experiment, epithelial cells from a nasal polyp of a CF patient were cultured on permeable filter supports. These cells form an electrically tight epithelial monolayer after several days in culture. Eight days after seeding, the cells were exposed to the Ad2/CFTR virus for 6 hours. Three days later, the short-circuit current (I_{sc}) across the monolayer was measured. cAMP agonists did not increase the I_{sc}, indicating that there was no change in chloride secretion. However, this defect was corrected after infection with recombinant Ad2/CFTR. Cells infected with Ad2/CFTR (MOI=5; MOI refers to multiplicity of infection; 1 MOI indicates one pfu/cell) express functional CFTR; cAMP agonists stimulated I_{sc}, indicating stimulation of Cl⁻ secretion. Ad2/CFTR also corrected the CF chloride channel defect in CF tracheal epithelial cells. Additional studies indicated that Ad2/CFTR was able to correct the chloride secretory defect without altering the transepithelial electrical resistance; this result indicates that the integrity of the epithelial cells and the tight junctions was not disrupted by infection with Ad2/CFTR. Application of 1 MOI of Ad2/CFTR was also found to be sufficient to correct the CF chloride secretory defect.

The experiments using primary cultures of human airway epithelial cells indicate that the Ad2/CFTR virus is able to enter CF airway epithelial cells and express sufficient CFTR to correct the defect in chloride transport.

20 Example 9 -In Vivo Delivery to and Expression of CFTR in Cotton Rat and Rhesus Monkey Epithelium

MATERIALS AND METHODS

Adenovirus vector

25 Ad2/CFTR-1 was prepared as described in Example 7. The DNA construct comprises a full length copy of the Ad2 genome of approximately 37.5 kb from which the early region 1 genes (nucleotides 546 to 3497) have been replaced by cDNA for CFTR (nucleotides 123 to 4622 of the published CFTR sequence with 53 additional linker nucleotides). The viral Ela promoter was used for CFTR cDNA. Termination/polyadenylation occurs at the site normally used by the Elb and protein IX transcripts. The recombinant virus E3 region was conserved. The size of the Ad2-CFTR-1 vector is approximately 104.5% that of wild-type adenovirus. The recombinant virus was grown in 293 cells that complement the E1 early viral promoters. The cells were frozen and thawed three times to release the virus and the preparation was purified on a CsCl gradient, then dialyzed against Tris-buffered saline (TBS) to remove the CsCl, as described.

Animals

Rats. Twenty two cotton rats (6-8 weeks old, weighing between 80-100 g) were used for this study. Rats were anesthetized by inhaled methoxyflurane (Pitman Moore, Inc., Mundelen, Ill). Virus was applied to the lungs by nasal instillation during inspiration.

5 Two cotton rat studies were performed. In the first study, seven rats were assigned to a one time pulmonary infection with 100 μ l solution containing 4.1×10^9 plaque forming units (pfu) of the Ad2/CFTR-1 virus and 3 rats served as controls. One control rat and either two or three experimental rats were sacrificed with methoxyflurane and studies at each of three time points: 4, 11, or 15 days after infection.

10 The second group of rats was used to test the effect of repeat administration of the recombinant virus. All 12 rats received 2.1×10^8 pfu of the Ad2/CFTR-1 virus on day 0 and 9 of the rats received a second dose of 3.2×10^8 pfu of Ad2/CFTR-1 14 days later. Groups of one control rat and three experimental rats were sacrificed at 3, 7, or 14 days after the second administration of virus. Before necropsy, the trachea was cannulated and
15 bronchoalveolar lavage (BAL) was performed with 3 ml aliquots of phosphate-buffered saline. A median sternotomy was performed and the right ventricle cannulated for blood collection. The right lung and trachea were fixed in 4% formaldehyde and the left lung was frozen in liquid nitrogen and kept at -70°C for evaluation by immunochemistry, reverse transcriptase polymerase chain reaction (RT-PCR), and viral culture. Other organs were removed and
20 quickly frozen in liquid nitrogen for evaluation by polymerase chain reaction (PCR).

Monkeys. Three female Rhesus monkeys were used for this study; a fourth female monkey was kept in the same room, and was used as control. For application of the virus, the monkeys were anesthetized by intramuscular injection of ketamine (15 mg/kg). The entire epithelium of one nasal cavity in each monkey was used for virus application. A foley
25 catheter (size 10) was inserted through each nasal cavity into the pharynx, the balloon was inflated with 2-3 ml of air, and then pulled anteriorly to obtain a tight occlusion at the posterior choana. The Ad2/CFTR-1 virus was then instilled slowly in the right nostril with the posterior balloon inflated. The viral solution remained in contact with the nasal mucosa for 30 min. The balloons were deflated, the catheters were removed, and the monkeys were
30 allowed to recover from anesthesia. A similar procedure was performed on the left nostril, except that TBS solution was instilled as a control. The monkeys received a total of three doses of the virus over a period of 5 months. The total dose given was 2.5×10^9 pfu the first time, 2.3×10^9 pfu the second time, and 2.8×10^9 pfu the third time. It was estimated that the cell density of the nasal epithelia to be 2×10^6 cells/cm² and a surface area of 25 to 50
35 cm². This corresponds to a multiplicity of infection (MOI) of approximately 25.

The animals were evaluated 1 week before the first administration of virus, on the day of administration, and on days 1, 3, 6, 13, 21, 27, and 42 days after infection. The second administration of virus occurred on day 55. The monkeys were evaluated on day 55 and then on days 56, 59, 62, 69, 76, 83, 89, 96, 103, and 111. For the third administration, on day 134,

only the left nostril was cannulated and exposed to the virus. The control monkey received instillations of PBS instead of virus. Biopsies of the left medial turbinate were carried out on day 135 in one of the infected monkeys, on day 138 on the second infected monkey, and on day 142 on the third infected monkey and on the control monkey.

5 For evaluations, monkeys were anesthetized by intramuscular injection of ketamine (15 mg/kg). To obtain nasal epithelial cells, the nasal mucosa was first impregnated with 5 drops of Afrin (0.05% oxymetazoline hydrochloride, Schering-Plough) and 1 ml of 2% Lidocaine for 5 minutes. A cytobrush was then used to gently rub the mucosa for about 3 sec. To obtain pharyngeal epithelial swabs, a cotton-tipped applicator was rubbed over the
10 back of the pharynx 2-3 times. The resulting cells were dislodged from brushes or applicators into 2 ml of sterile PBS. Biopsies of the medial turbinate were performed using cupped forceps under direct endoscopic control.

Animals were evaluated daily for evidence of abnormal behavior of physical signs. A record of food and fluid intake was used to assess appetite and general health. Stool
15 consistency was also recorded to check for the possibility of diarrhea. At each of the evaluation time points, rectal temperature, respiratory rate, and heart rate were measured. The nasal mucosa, conjunctivas, and pharynx were visually inspected. The monkeys were also examined for lymphadenopathy.

Venous blood from the monkeys was collected by standard venipuncture technique.
20 Blood/serum analysis was performed in the clinical laboratory of the University of Iowa Hospitals and Clinics using a Hitachi 737 automated chemistry analyzer and a Technicom H6 automated hematology analyzer.

Serology

25 Sera were obtained and anti-adenoviral antibody titers were measured by an enzyme-linked immunoadsorbant assay (ELISA). For the ELISA, 50 ng/well of filled adenovirus (Lee Biomolecular Research Laboratories, San Diego, Ca) in 0.1M NaHCO₃ were coated on 96 well plates at 4°C overnight. The test samples at appropriate dilutions were added, starting at a dilution of 1/50. The samples were incubated for 1 hour, the plates washed, and
30 a goat anti-human IgG HRP conjugate (Jackson ImmunoResearch Laboratories, West Grove, PA) was added and incubated for 1 hour. The plates were washed and O-Phenylenediamine (Sigma Chemical Co., St. Louis, MO) was added for 30 min. at room temperature. The assay was stopped with 4.5 M H₂SO₄ and read at 490 nm on a Molecular Devices microplate reader. The titer was calculated as the product of the reciprocal of the initial dilution and the
35 reciprocal of the dilution in the last well with an OD>0.100.

Neutralizing antibodies measure the ability of the monkey serum to prevent infection of 293 cells by adenovirus. Monkey serum (1:25 dilution) [or nasal washings (1:2 dilutions)] was added in two-fold serial dilutions to a 96 well plate. Adenovirus (2.5 x 10⁵ pfu) was added and incubated for 1 hour at 37°C. The 293 cells were then added to all wells and the

plates were incubated until the serum-free control wells exhibited >95% cytopathic effect. The titer was calculated as the product of the reciprocal of the initial dilution times the reciprocal of the dilution in the last well showing >95% cytopathic effect.

5 Bronchoalveolar lavage and nasal brushings for cytology

Bronchoalveolar lavage (BAL) was performed by cannulating the trachea with a silastic catheter and injecting 5 ml of PBS. Gentle suction was applied to recover the fluid. The BAL sample was spun at 5000 rpm for 5 min. and cells were resuspended in 293 media at a concentration of 10^6 cells/ml. Cells were obtained from the monkey's nasal epithelium
10 by gently rubbing the nasal mucosa for about 3 sec. with a cytobrush. The resulting cells were dislodged from the brushes into 2 ml of PBS. Forty microliters of the cell suspension were cytocentrifuged onto slides and stained with Wright's stain. Samples were examined by light microscopy.

15

Histology of lung sections and nasal biopsies

The right lung of each cotton rat was removed, inflated with 4% formaldehyde, and embedded in paraffin for sectioning. Nasal biopsies from the monkeys were also fixed with 4% formaldehyde. Histologic sections were stained with hematoxylin and eosin (H&E).
20 Sections were reviewed by at least one of the study personnel and by a pathologist who was unaware of the treatment each rat received.

Immunocytochemistry

Pieces of lung and trachea of the cotton rats and nasal biopsies were frozen in liquid
25 nitrogen on O.C.T. compound. Cryosections and paraffin sections of the specimens were used for immunofluorescence microscopy. Cytospin slides of nasal brushings were prepared on gelatin coated slides and fixed with paraformaldehyde. The tissue was permeabilized with Triton X-100, then a pool of monoclonal antibodies to CFTR (M13-1, M1-4) (Denning, G.M. et al. (1992) *J. Clin. Invest.* 89:339-349) was added and incubated for 12 hours. The primary
30 antibody was removed and an anti-mouse biotinylated antibody (Biomed, Foster City, CA) was added. After removal of the secondary antibody, streptavidin FITC (Biomed, Foster City, Ca) was added and the slides were observed under a laser scanning confocal microscope. Both control animal samples and non-immune IgG stained samples were used as controls.

35

PCR

PCR was performed on pieces of small bowel, brain, heart, kidney, liver, ovaries, and spleen from cotton rats. Approximately 1 g of the rat organs was mechanically ground and mixed with 50 μ l sterile water, boiled for 5 min., and centrifuged. A 5 μ l aliquot of the

supernatant was removed for further analysis. Monkey nasal brushings suspensions were also used for PCR.

Nested PCR primer sets were designed to selectively amplify Ad2/CFTR-1 DNA over endogenous CFTR by placing one primer from each set in the adenovirus sequence and the other primer in the CFTR sequence. The first primer set amplifies a 723 bp fragment and is shown below:

Ad2 5' ACT CTT GAG TGC CAG CGA GTA GAG TTT TCT CCT CCG 3' (SEQ ID NO:4)

CFTR 5' GCA AAG GAG CGA TCC ACA CGA AAT GTG CC 3' (SEQ ID NO:5)

The nested primer set amplifies a 506 bp fragment and is shown below:

Ad2 5' CTC CTC CGA GCC GCT CCG AGC TAG 3' (SEQ ID NO:6)

CFTR 5' CCA AAA ATG GCT GGG TGT AGG AGC AGT GTC C 3' (SEQ ID NO:7)

A PCR reaction mix containing 10mM Tris-Cl (pH 8.3), 50mM KCl, 1.5 mM MgCl₂, 0.001% (w/v) gelatin, 400 µM each dNTP, 0.6 µM each primer (first set), and 2.5 units AmpliTaq (Perkin Elmer) was aliquoted into separate tubes. A 5 µl aliquot of each sample prep was then added and the mixture was overlaid with 50 µl of light mineral oil. The samples were processed on a Barnstead/Thermolyne (Dubuque, IA) thermal cycler programmed for 1 min. at 94°C, 1 min. at 65°C, and 2 min. at 72°C for 40 cycles. Post-run dwell was for 7 min. at 72°C. A 5 µl aliquot was removed and added to a second PCR reaction using the nested set of primers and cycled as above. A 10 µl aliquot of the final amplification reaction was analyzed on a 1% agarose gel and visualized with ethidium bromide.

To determine the sensitivity of this procedure, a PCR mix containing control rat liver supernatant was aliquoted into several tubes and spiked with dilutions of Ad2/CFTR-1. Following the amplification protocols described above, it was determined that the nested PCR procedure could detect as little as 50 pfu of viral DNA.

RT-PCR

RT-PCR was used to detect vector-generated mRNA in cotton rat lung tissue and samples from nasal brushings from monkeys. A 200 µl aliquot of guanidine isothiocyanate solution (4 M guanidine isothiocyanate, 25 mM sodium citrate pH 7.0, 0.5% sarcosyl, and 0.1 M β-mercaptoethanol) was added to a frozen section of each lung and pellet from nasal brushings and the tissue was mechanically ground. Total RNA was isolated utilizing a single-step method (Chomczynski, P. and Sacchi, N. et al. (1987) *Analytical Biochemistry* 162:156-159; Hanson, C.A. et al. (1990) *Am. J. Pathol.* 137:1-6). The RNA was incubated with 1 unit RQ1 RNase-free DNase (Promega Corp., Madison WI) at 37°C for 20 min., denatured at 99°C for 5 min., precipitated with ammonium acetate and ethanol, and redissolved in 4 µl diethylpyrocarbonate treated water containing 20 units RNase Block 1 (Stratagene, La Jolla CA). A 2 µl aliquot of the purified RNA was reverse transcribed using

the GeneAmp RNA PCR kit (Perkin Elmer Cetus) and the downstream primer from the first primer set described in the previous section. Reverse transcriptase was omitted from the reaction with the remaining 2 µl of the purified RNA prep, as a control in which preparations (both +/- RT) were then amplified using nested primer sets and the PCR protocols described above. A 10 µl aliquot of the final amplification reaction was analyzed on a 1% agarose gel and visualized with ethidium bromide.

Southern analysis.

To verify the identity of the PCR products, Southern analysis was performed. The DNA was transferred to a nylon membrane as described (Sambrook *et al.*, *supra*). A fragment of CFTR cDNA (amino acids #1-525) was labeled with [³²P]-dCTP (ICN Biomedicals, Inc. Irvine CA) using an oligolabeling kit (Pharmacia, Piscataway, NJ) and purified over a NICK column (Pharmacia Piscataway, NJ) for use as a hybridization probe. The labeled probe was denatured, cooled, and incubated with the prehybridized filter for 15 hours at 42°C. The hybridized filter was then exposed to film (Kodak XAR-5) for 10 min.

Culture of Ad2/CFTR-1

Viral cultures were performed on the permissive 293 cell line. For culture of virus from lung tissue, 1 g of lung was frozen/thawed 3-6 times and then mechanically disrupted in 200 µl of 293 media. For culture of BAL and monkey nasal brushings, the cell suspension was spun for 5 min and the supernatant was collected. Fifty µl of the supernatant was added in duplicate to 293 cells grown in 96 well plates at 50% confluence. The 293 cells were incubated for 72 hr at 37°C, then fixed with a mixture of equal parts of methanol and acetone for 10 min. and incubated with FITC-labeled anti-adenovirus monoclonal antibodies (Chemicon, Light Diagnostics, Temecuca, CA) for 30 min. Positive nuclear immunofluorescence was interpreted as positive culture. The sensitivity of the assay was evaluated by adding dilutions of Ad2/CFTR-1 to 50 µl of the lung homogenate from one of the control rats. Viral replication was detected when as little as 1 pfu was added.

RESULTS

Efficacy of Ad2/CFTR-1 in the lungs of cotton rats.

To test the ability of Ad2/CFTR-1 to transfer CFTR cDNA to the intrapulmonary airway epithelium, several studies were performed. 4 x 10⁶ pfu - IU of Ad2/CFTR-1 in 100 µl was administered to seven cotton rats; three control rats received 100 µl of TBS (the vehicle for the virus). The rats were sacrificed 4, 10 or 14 days later. To detect viral transcripts encoding CFTR, reverse transcriptase was used to prepare cDNA from lung homogenates. The cDNA was amplified with PCR using primers that span adenovirus and CFTR-encoded

sequences. Thus, the procedure did not detect endogenous rat CFTR. Figure 16 shows that the lungs of animals which received Ad2/CFTR-1 were positive for virally-encoded CFTR mRNA. The lungs of all control rats were negative.

To detect the protein, lung sections were immunostained with antibodies specific to CFTR. CFTR was detected at the apical membrane of bronchial epithelium from all rats exposed to Ad2/CFTR-1, but not from control rats. The location of recombinant CFTR at the apical membrane is consistent with the location of endogenous CFTR in human airway epithelium. Recombinant CFTR was detected above background levels because endogenous levels of CFTR in airway epithelia are very low and thus, difficult to detect by immunocytochemistry (Trapnell, B. et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:6565-6569; Denning, G.M. et al. (1992) *J. Cell Biol.* 118:551-59).

These results show that Ad2/CFTR-1 directs the expression of CFTR mRNA in the lung of the cotton rat and CFTR protein in the intrapulmonary airways.

15 Safety of Ad2/CFTR-1 in cotton rats.

Because the E1 region of Ad2 is deleted in the Ad2/CFTR-1 virus, the vector was expected to be replication-impaired (Berkner, K.L. (1988) *BioTechniques* 6:616-629) and that it would be unable to shut off host cell protein synthesis (Basuss, L.E. et al. (1989) *J. Virol.* 50:202-212). Previous *in vitro* studies have suggested that this is the case in a variety of cells including primary cultures of human airway epithelial cells (Rich, D.P. et al. (1993) *Human Gene Therapy* 4:461-476). However, it is important to confirm this *in vivo* in the cotton rat, which is the most permissive animal model for human adenovirus infection (Ginsberg, H.S. et al. (1989) *Proc. Natl. Acad. Sci. USA* 86:3823-3827; Prince, G.A. et al. (1993) *J. Virol* 67:101-111). Although dose of virus of 4.1×10^{10} pfus per kg was used, none of the rats died. More importantly, extracts from lung homogenates from each of the cotton rats were cultured in the permissive 293 cell line. With this assay 1 pfu of recombinant virus was detected in lung homogenate. However, virus was not detected by culture in the lungs of any of the treated animals. Thus, the virus did not appear to replicate *in vivo*.

It is also possible that administration of Ad2/CFTR-1 could cause an inflammatory response, either due to a direct effect of the virus or as a result of administration of viral particles. Several studies were performed to test this possibility. None of the rats had a change in the total or differential white blood cell count, suggesting that there was no major systemic inflammatory response. To assess the pulmonary inflammatory response more directly, bronchoalveolar lavage was performed on each of the rats (Figures 17A and 17B). Figure 17A shows that there was no change in the total number of cells recovered from the lavage or in the differential cell count.

Sections of the lung stained by H&E were also prepared. There was no evidence of viral inclusions or any other changes characteristic of adenoviral infection (Prince, G.A. et al. (1993) *J. Virol.* 67:101-111). When coded lung sections were evaluated by a skilled reader

who was unaware of which sections were treated, she was unable to distinguish between sections from the treated and untreated lungs.

It seemed possible that the recombinant adenovirus could escape from the lung into other tissues. To test for this possibility, other organs from the rats were evaluated using
5 nested PCR to detect viral DNA. All organs tested from infected rats were negative, with the exception of small bowel which was positive in 3 of 7 rats. Figure 18 shows the results of 2 infected rats and one control rat sacrificed on day 4 after infection. The organ homogenates from the infected rats sacrificed were negative for Ad2/CFTR-1 with the exception of the small bowel. Organ homogenates from control rats sacrificed on day 4 after infection were
10 negative for Ad2/CFTR-1. The presence of viral DNA in the small bowel suggests that the rats may have swallowed some of the virus at the time of instillation or, alternatively, the normal airway clearance mechanisms may have resulted in deposition of viral DNA in the gastrointestinal tract. Despite the presence of viral DNA in homogenates of small intestine, none of the rats developed diarrhea. This result suggests that if the virus expressed CFTR in
15 the intestinal epithelium, there was no obvious adverse consequence.

Repeat administration of Ad2/CFTR-1 to cotton rats

Because adenovirus DNA integration into chromosomal DNA is not necessary for gene expression and only occurs at very low frequency, expression following any given
20 treatment was anticipated to be finite and that repeated administration of recombinant adenovirus would be required for treatment of CF airway disease. Therefore, the effect of repeated administration of Ad2/CFTR-1 cotton rats was examined. Twelve cotton rats received 50 µl of Ad2/CFTR-1. Two weeks later, 9 of the rats received a second dose of 50 µl of Ad2/CFTR-1 and 3 rats received 50 µl of TBS. Rats were sacrificed on day 3, 7, or 14
25 after virus administration. At the time of the second vector administration all cotton rats had an increased antibody titer to adenovirus.

After the second intrapulmonary administration of virus, none of the rats died. Moreover, the results of studies assessing safety and efficacy were similar to results obtained in animals receiving adenovirus for the first time. Viral cultures of rat lung homogenates on
30 293 cells were negative at all time points, suggesting that there was no virus replication. There was no difference between treated and control rats in the total or differential white blood count at any of the time points. The lungs were evaluated by histologic sections stained with H&E; and found no observable differences between the control and treated rats when sections were read by us or by a blinded skilled reader. Examples of some sections are
35 shown in Figure 19. When organs were examined for viral DNA using PCR, viral DNA was found only in the small intestine of 2 rats. Despite seropositivity of the rats at the time of the second administration, expression of CFTR (as assessed by RT-PCR and by immunocytochemistry of sections stained with CFTR antibodies) similar to that seen in animals that received a single administration was observed.

These results suggest that prior administration of Ad2/CFTR-1 and the development of an antibody response did not cause an inflammatory response in the rats nor did it prevent virus-dependent production of CFTR.

5 Evidence that Ad2/CFTR-1 expresses CFTR in primate airway epithelium

The cells lining the respiratory tract and the immune system of primates are similar to those of humans. To test the ability of Ad2/CFTR-1 to transfer CFTR to the respiratory epithelium of primates, Ad2/CFTR was applied on three occasions as described in the methods to the nasal epithelium of three Rhesus monkeys. To obtain cells from the
10 respiratory epithelium, the epithelium was brushed using a procedure similar to that used to sample the airway epithelium of humans during fiberoptic bronchoscopy.

To assess gene transfer, RT-PCR was used as described above for the cotton rats. RT-PCR was positive on cells brushed from the right nostril of all three monkeys, although it was only detectable for 18 days after virus administration. An example of the results are
15 shown in Figure 20A. The presence of a positive reaction in cells from the left nostril most likely represents some virus movement to the left side due to drainage, or possibly from the monkey moving the virus from one nostril to the other with its fingers after it recovered from anesthesia.

The specificity of the RT-PCR is shown in Figure 20B. A Southern blot with a probe
20 to CFTR hybridized with the RT-PCR product from the monkey infected with Ad2/CFTR-1. As a control, one monkey received a different virus (Ad2/ β Gal-1) which encodes β -galactosidase. When different primers were used to reverse transcribe the β -galactosidase mRNA and amplify the cDNA, the appropriate PCR product was detected. However, the PCR product did not hybridize to the CFTR probe on Southern blot. This result shows the
25 specificity of the reaction for amplification of the adenovirus-directed CFTR transcript.

The failure to detect evidence of adenovirus-encoded CFTR mRNA at 18 days or beyond suggests that the sensitivity of the RT-PCR may be low because of limited efficacy of the reverse transcriptase or because RNases may have degraded RNA after cell acquisition. Viral DNA, however, was detected by PCR in brushings from the nasal epithelium for
30 seventy days after application of the virus. This result indicates that although mRNA was not detected after 2 weeks, viral DNA was present for a prolonged period and may have been transcriptionally active.

To assess the presence of CFTR proteins directly, cells obtained by brushing were plated onto slides by cytopspin and stained with antibodies to CFTR. Figure 21 shows an
35 example of the immunocytochemistry of the brushed cells. A positive reaction is clearly evident in cells exposed to Ad2/CFTR-1. The cells were scored as positive by immunocytochemistry when evaluated by a reader uninformed to the identity of the samples. Immunocytochemistry remained positive for five to six weeks for the three monkeys, even after the second administration of Ad2/CFTR-1. On occasion, a few positive staining cells

were observed from the contralateral nostril of the monkeys. However, this was of short duration, lasting at most one week.

Sections of nasal turbinate biopsies obtained within a week after the third infection were also examined. In sections from the control monkey, little if any immunofluorescence from the surface epithelium was observed, but the submucosal glands showed significant staining of CFTR (Fig. 22). These observations are consistent with results of previous studies (Engelhardt, J.F. and Wilson, J.M. (1992) *Nature Gen.* 2:240-248.) In contrast, sections from monkeys that received Ad2/CFTR-1 revealed increased immunofluorescence at the apical membrane of the surface epithelium. The submucosal glands did not appear to have greater immunostaining than was observed under control conditions. These results indicate that Ad2/CFTR-1 can transfer the CFTR cDNA to the airway epithelium of Rhesus monkeys, even in seropositive animals (see below).

Safety of Ad2/CFTR-1 administered to monkeys

Figure 23 shows that all three treated monkeys developed antibodies against adenovirus. Antibody titers measured by ELISA rose within two weeks after the first infection. With subsequent infections the titer rose within days. The sentinel monkey had low antibody titers throughout the experiment. Tests for the presence of neutralizing antibodies were also performed. After the first administration, neutralizing antibodies were not observed, but they were detected after the second administration and during the third viral administration (Fig. 23).

To detect virus, supernatants from nasal brushings and swabs were cultured on 293 cells. All monkeys had positive cultures on day 1 and on day 3 or 4 from the infected nostril. Cultures remained positive in one of the monkeys at seven days after administration, but cultures were never positive beyond 7 days. Live virus was occasionally detected in swabs from the contra lateral nostril during the first 4 days after infection. The rapid loss of detectable virus suggests that there was not viral replication. Stools were routinely cultured, but virus was never detected in stools from any of the monkeys.

None of the monkeys developed any clinical signs of viral infection or inflammation. Visual inspection of the nasal epithelium revealed slight erythema in all three monkeys in both nostrils on the first day after infection; but similar erythema was observed in the control monkey and likely resulted from the instrumentation. There was no visible abnormalities at days 3 or 4, or on weekly inspection thereafter. Physical examination revealed no fever, lymphadenopathy, conjunctivitis, tachypnea, or tachycardia at any of the time points. No abnormalities were found in a complete blood count or sedimentation rate, nor were abnormalities observed in serum electrolytes, transaminases, or blood urea nitrogen and creatinine.

Examination of Wright-stained cells from the nasal brushings showed that neutrophils and lymphocytes accounted for less than 5% of total cells in all three monkeys.

Administration of the Ad2/CFTR-1 caused no change in the distribution or number of inflammatory cells at any of the time points following virus administration. H&E stains of the nasal turbinate biopsies specimens from the control monkey could not be differentiated from that of the experimental monkey when the specimens were reviewed by an independent pathologist. (Fig. 24)

These results demonstrate the ability of a recombinant adenovirus encoding CFTR (Ad2/CFTR-1) to express CFTR cDNA in the airway epithelium of cotton rats and monkeys during repeated administration. They also indicate that application of the virus involves little if any risk. Thus, they suggest that such a vector may be of value in expressing CFTR in the airway epithelium of humans with cystic fibrosis.

Two methods were used to show that Ad2/CFTR-1 expresses CFTR in the airway epithelium of cotton rats and primates: CFTR mRNA was detected using RT-PCR and protein was detected by immunocytochemistry. Duration of expression as assessed immunocytochemically was five to six weeks. Because very little protein is required to generate Cl^- secretion (Welsh, M.J. (1987) *Physiol. Rev.* 67:1143-1184; Trapnell, B.C. et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:6565-6569; Denning, G.M. et al. (1992) *J. Cell Biol.* 118:551-559), it is likely that functional expression of CFTR persists substantially longer than the period of time during which CFTR was detected by immunocytochemistry. Support for this evidence comes from two considerations: first, it is very difficult to detect CFTR immunocytochemically in the airway epithelium, yet the expression of an apical membrane Cl^- permeability due to the presence of CFTR Cl^- channels is readily detected. The ability of a minimal amount of CFTR to have important functional effects is likely a result of the fact that a single ion channel conducts a very large number of ions ($10^6 - 10^7$ ions/sec). Thus, ion channels are not usually abundant proteins in epithelia. Second, previous work suggests that the defective electrolyte transport of CF epithelia can be corrected when only 6-10% of cells in a CF airway epithelium overexpress wild-type CFTR (Johnson, L.G. et al. (1992) *Nature Gen.* 2:21-25). Thus, correction of the biologic defect in CF patients may be possible when only a small percent of the cells express CFTR. This is also consistent with our previous studies *in vitro* showing that Ad2/CFTR-1 at relatively low multiplicities of infection generated a cAMP-stimulated Cl^- secretory response in CF epithelia (Rich, D.P. et al. (1993) *Human Gene Therapy* 4:461-476).

This study also provides the first comprehensive data on the safety of adenovirus vectors for gene transfer to airway epithelium. Several aspects of the studies are encouraging. There was no evidence of viral replication, rather infectious viral particles were rapidly cleared from both cotton rats and primates. These data, together with our previous *in vitro* studies, suggest that replication of recombinant virus in humans will likely not be a problem. The other major consideration for safety of an adenovirus vector in the treatment of CF is the possibility of an inflammatory response. The data indicate that the virus generated an antibody response in both cotton rats and monkeys. Despite this, no evidence of a

systemic or local inflammatory response was observed. The cells obtained by bronchoalveolar lavage and by brushing and swabs were not altered by virus application. Moreover, the histology of epithelia treated with adenovirus was indistinguishable from that of control epithelia. These data suggest that at least three sequential exposures of airway epithelium to adenovirus does not cause a detrimental inflammatory response.

These data suggest that Ad2/CFTR-1 can effectively transfer CFTR cDNA to airway epithelium and direct the expression of CFTR. They also suggest that transfer is relatively safe in animals. Thus, they suggest that Ad2/CFTR-1 may be a good vector for treating patients with CF. This was confirmed in the following example.

Example 10 - CFTR Gene Therapy in Nasal Epithelia from Human CF Subjects

EXPERIMENTAL PROCEDURES

Adenovirus vector

The recombinant adenovirus Ad2/CFTR-1 was used to deliver CFTR cDNA. The construction and preparation of Ad2/CFTR-1, and its use *in vitro* and *in vivo* in animals, has been previously described (Rich, D.P. et al. (1993) *Human Gene Therapy* 4:461-476; Zabner, J. et al. (1993) *Nature Gen.* (in press)). The DNA construct comprises a full length copy of the Ad2 genome from which the early region 1 genes (nucleotides 546 to 3497) have been replaced by cDNA for CFTR. The viral E1a promoter was used for CFTR cDNA; this is a low to moderate strength promoter. Termination/polyadenylation occurs at the site normally used by E1b and protein IX transcripts. The E3 region of the virus was conserved.

Patients

Three patients with CF were studied. Genotype was determined by IG Labs (Framingham, MA). All three patients had mild CF as defined by an NIH score > 70 (Taussig, L.M. et al. (1973) *J. Pediatr.* 82:380-390), a normal weight for height ratio, a forced expiratory volume in one second (FEV1) greater than 50% of predicted and an arterial PO₂ greater than 72. All patients were seropositive for type 2 adenovirus, and had no recent viral illnesses. Pretreatment cultures of nasal swabs, pharyngeal swabs, sputum, urine, stool, and blood leukocytes were negative for adenovirus. PCR of pretreatment nasal brushings using primers for the adenovirus E1 region were negative. Patients were evaluated at least twice by FEV1, cytology of nasal mucosa, visual inspection, and measurement of V_T before treatment. Prior to treatment, a coronal computed tomographic scan of the paranasal sinuses and a chest X-ray were obtained.

The first patient was a 21 year old woman who was diagnosed at 3 months after birth. She had pancreatic insufficiency, a positive sweat chloride test (101 mEq/l), and is homozygous for the $\Delta F508$ mutation. Her NIH score was 90 and her FEV1 was 83%

predicted. The second patient was a 36 year old man who was diagnosed at the age of 13 when he presented with symptoms of pancreatic insufficiency. A sweat chloride test revealed a chloride concentration of 70 mEq/l. He is a heterozygote with the $\Delta F508$ and G551D mutations. His NIH score was 88 and his FEV1 was 66% predicted. The third patient was a
5 50 year old woman, diagnosed at the age of 9 with a positive sweat chloride test (104 mEq/l). She has pancreatic insufficiency and insulin dependent diabetes mellitus. She is homozygous for the $\Delta F508$ mutation. Her NIH score was 73 and her FEV1 was 65% predicted.

Transepithelial voltage

10 The transepithelial electric potential difference across the nasal epithelium was measured using techniques similar to those previously described (Alton, E.W.F.W. et al (1987) *Thorax* 42:815-817; Knowles, M. et al. (1981) *N. Eng. J. Med.* 305:1489-1495). A 23 gauge subcutaneous needle connected with sterile normal saline solution to a silver/silver chloride pellet (E.W. Wright, Guilford, CT) was used as a reference electrode. The exploring
15 electrode was a size 8 rubber catheter (modified Argyle^R Foley catheter, St. Louis, MO) with one side hole at the tip. The catheter was filled with Ringer's solution containing (in mM), 135 NaCl, 2.4 KH₂PO₄, K₂HPO₄, 1.2CaCl₂, 1.2 MgCl₂ and 10 Hepes (titrated to pH 7.4 with NaOH) and was connected to a silver/silver chloride pellet. Voltage was measured with a voltmeter (Keithley Instruments Inc., Cleveland, OH) connected to a strip chart recorder
20 (Servocorder, Watanabe Instruments, Japan). Prior to the measurements, the silver/silver chloride pellets were connected in series with the Ringer's solution; the pellets were changed if the recorded V_t was greater than ± 4 mV. The rubber catheter was introduced into the nostril under telescopic guidance (Hopkins Telescope, Karl Storz, Tuttlingen West Germany) and the side hole of the catheter was placed next to the study area in the medical aspect of the
25 inferior nasal turbinate. The distance from the anterior tip of the inferior turbinate and the spatial relationship with the medial turbinate, the maxillary sinus ostium, and in one patient a small polyp, were used to locate the area of Ad2/CFTR-1 administration for measurements. Photographs and video recorder images were also used. Basal V_t was recorded until no changes in V_t were observed after slow intermittent 100 μ l/min infusion of the Ringer's
30 solution. Once a stable baseline was achieved, 200 μ l of a Ringer's solution containing 100 μ M amiloride (Merck and Co. Inc., West Point, PA) was instilled through the catheter and changes in V_t were recorded until no further change were observed after intermittent instillations. Finally, 200 μ l Ringer's solution containing 100 μ M amiloride plus 10 μ M terbutaline (Geigy Pharmaceuticals, Ardsley, NY) was instilled and the changes in V_t were
35 recorded.

Measurements of basal V_t were reproducible over time: in the three treated patients, the coefficients of variation before administration of Ad2/CFTR-1 were 3.6%, 12%, and 12%. The changes induced by terbutaline were also reproducible. In 30 measurements in 9 CF patients, the terbutaline-induced changes in V_t (ΔV_t) ranged from 0 mV to +4 mV;

hyperpolarization of V_t was never observed. In contrast, in 7 normal subjects ΔV_t ranged from -1 mV to -5 mV; hyperpolarization was always observed.

Ad2/CFTR-1 application and cell acquisition

5 The patients were taken to the operating room and monitoring was commenced using continuous EKG and pulse oximetry recording as well as automatic intermittent blood pressure measurement. After mild sedation, the nasal mucosa was anesthetized by atomizing 0.5 ml of 5% cocaine. The mucosa in the area of the inferior turbinate was then packed with cotton pledgets previously soaked in a mixture of 2 ml of 0.1% adrenaline and 8 ml of 1% tetracaine. The pledgets remained in place for 10-40 min. Using endoscopic visualization with a television monitoring system, the applicator was introduced through the nostril and positioned on the medial aspect of the inferior turbinate, at least three centimeters from its anterior tip (Figures 25A-25I). The viral suspension was infused into the applicator through connecting catheters. The position of the applicator was monitored endoscopically to ensure that it did not move and that enough pressure was applied to prevent leakage. After the virus was in contact with the nasal epithelium for thirty minutes, the viral suspension was removed, and the applicator was withdrawn. In the third patient's right nasal cavity, the virus was applied using the modified Foley catheter used for V_t measurements. The catheter was introduced without anesthetic under endoscopic guidance until the side hole of the catheter was in contact with the area of interest in the inferior turbinate. The viral solution was infused slowly until a drop of solution was seen with the telescope. The catheter was left in place for thirty minutes and then removed.

Cells were obtained from the area of virus administration approximately 2 weeks before treatment and then at weekly intervals after treatment. The inferior turbinate was packed for 10 minutes with cotton pledgets previously soaked in 1 ml of 5% cocaine. Under endoscopic control, the area of administration was gently brushed for 5 seconds. The brushed cells were dislodged in PBS. Swabs of the nasal epithelia were collected using cotton tipped applicators without anesthesia. Cytospin slides were prepared and stained with Wright's stain. Light microscopy was used to assess the respiratory epithelial cells and inflammatory cells. For biopsies, sedatives/anesthesia was administered as described for the application procedure. After endoscopic inspection, and identification of the site to be biopsied, the submucosa was injected with 1% xylocaine, with 1/100,000 epinephrine. The area of virus application on the inferior turbinate was removed. The specimen was fixed in 4% formaldehyde and stained.

RESULTS

On day one after Ad2/CFTR-1 administration and at all subsequent time points, Ad2/CFTR-1 from the nasal epithelium, pharynx, blood, urine, or stool could not be cultured. As a control for the sensitivity of the culture assay, samples were routinely spiked with 10

and 100 IU Ad2/CFTR-1. In every case, the spiked samples were positive, indicating that, at a minimum, 10 IU of Ad2/CFTR should have been detected. No evidence of a systemic response as assessed by history, physical examination, serum chemistries or cell counts, chest and sinus X-rays, pulmonary function tests, or arterial blood gases performed before and after
5 Ad2/CFTR-1 administration. An increase in antibodies to adenovirus was not detectable by ELISA or by neutralization for 35 days after treatment.

Three to four hours after Ad2/CFTR-1 administration, at the time that local anesthesia and localized vasoconstriction abated, all patients began to complain of nasal congestion and in one case, mild rhinorrhea. These were isolated symptoms that diminished by 18 hours and
10 resolved by 28 to 42 hours. Inspection of the nasal mucosa showed mild to moderate erythema, edema, and exudate (Figures 25A-25C). These physical findings followed a time course similar to the symptoms. The physical findings were not limited to the site of virus application, even though preliminary studies using the applicator showed that marker methylene blue was limited to the area of application. In two additional patients with CF, the
15 identical anesthesia and application procedure were used, but saline was applied instead of virus, yet the same symptoms and physical findings were observed in these patients (Figures 25G-25I). Moreover, the local anesthesia and vasoconstriction generated similar changes even when the applicator was not used, suggesting that the anesthesia/vasoconstriction caused some, if not all the injury. Twenty-four hours after the application procedure, analysis of
20 cells removed from nasal swabs revealed an equivalent increase in the percent neutrophils in patients treated with Ad2/CFTR-1 or with saline. One week after application, the neutrophilia had resolved in both groups. Respiratory epithelial cells obtained by nasal brushing appeared normal at one week and at subsequent time points, and showed no evidence of inclusion bodies. To further evaluate the mucosa, the epithelium was biopsied on
25 day three in the first patient and day one in the second patient. Independent evaluation by two pathologists not otherwise associated with the study suggested changes consistent with mild trauma and possible ischemia (probably secondary to the anesthetic/vasoconstrictors used before virus administration), but there were no abnormalities suggestive of virus-mediated damage.

30 Because the application procedure produced some mild injury in the first two patients, the method of administration was altered in the third patient. The method used did not require the use of local anesthesia or vasoconstriction and which was thus less likely to cause injury, but which was also less certain in its ability to constrain Ad2/CFTR-1 in a precisely defined area. On the right side, Ad2/CFTR-1 was administered as in the first two patients,
35 and on the left side, the virus was administered without anesthesia or the applicator, instead using a small Foley catheter to apply and maintain Ad2/CFTR-1 in a relatively defined area by surface tension (Figure 25E). On the right side, the symptoms and physical findings were the same as those observed in the first two patients. By contrast, on the left side there were no symptoms and on inspection the nasal mucosa appeared normal (Figures 25D-25F). Nasal

swabs obtained from the right side showed neutrophilia similar to that observed in the first two patients. In contrast, the left side which had no anesthesia and minimal manipulation, did not develop neutrophilia. Biopsy of the left side on day 3 after administration (Figure 26), showed morphology consistent with CF-- a thickened basement membrane and
 5 occasional polymorphonuclear cells in the submucosa-- but no abnormalities that could be attributed to the adenovirus vector.

The first patient developed symptoms of a sore throat and increased cough that began three weeks after treatment and persisted for two days. Six weeks after treatment she developed an exacerbation of her bronchitis/bronchiectasis and hemoptysis that required
 10 hospitalization. The second patient had a transient episode of minimal hemoptysis three weeks after treatment; it was not accompanied by any other symptoms before or after the episode. The third patient has an exacerbation of bronchitis three weeks after treatment for which she was given oral antibiotics. Based on each patient's pretreatment clinical history, evaluation of the episodes, and viral cultures, no evidence could be discerned that linked
 15 these episodes to administration of Ad2/CFTR-1. Rather the episodes appeared consistent with the normal course of disease in each individual.

The loss of CFTR Cl^- channel function causes abnormal ion transport across affected epithelia, which in turn contributes to the pathogenesis of CF-associated airway disease (Boat, T.F. et al. in *The Metabolic Basis of Inherited Diseases* (Scriver, C.R. et al. eds.,
 20 McGraw-Hill, New York (1989); Quinton, P.M. (1990) *FASEB J.* 4:2709-2717). In airway epithelia, ion transport is dominated by two electrically conductive processes: amiloride-sensitive absorption of Na^+ from the mucosal to the submucosal surface and cAMP-stimulated Cl^- secretion in the opposite direction. (Quinton, P.M. (1990) *FASEB J.* 4:2709-2717; Welsh, M.J. (1987) *Physiol. Rev.* 67:1143-1184). These two transport processes can be
 25 assessed noninvasively by measuring the voltage across the nasal epithelium (V_t) *in vivo* (Knowles, M. et al (1981) *N. Eng. J. Med.* 305:1489-1495; Alton, E.W.F.W. et al.(1987) *Thorax* 42:815-817). Figure 27 shows an example from a normal subject. Under basal conditions, V_t was electrically negative (lumen referenced to the submucosal surface). Perfusion of amiloride (100 μM) onto the mucosal surface inhibited V_t by blocking apical
 30 Na^+ channels (Knowles, M. et al (1981) *N. Eng. J. Med.* 305:1489-1495; Quinton, P.M. (1990) *FASEB J.* 4:2709-2717; Welsh, M.J. (1992) *Neuron* 8:821-829). Subsequent perfusion of terbutaline (10 μM) a β -adrenergic agonist, hyperpolarized V_t by increasing cellular levels of cAMP, opening CFTR Cl^- channels, and stimulating chloride secretion (Quinton, P.M. (1990) *FASEB J.* 4:2709-2717; Welsh, M.J. et al. (1992) *Neuron* 8:821-829).
 35 Figure 28A shows results from seven normal subjects: basal V_t was $-10.5 \pm 1.0\text{mV}$, and in the presence of amiloride, terbutaline hyperpolarized V_t by $-2.3 \pm 0.5\text{mV}$.

In patients with CF, V_t was more electrically negative than in normal subjects (Figure 28B), as has been previously reported (Knowles, M. et al. (1981) *N. Eng. J. Med.* 305:1489-1495). Basal V_t was $-37.0 \pm 2.4\text{mV}$, much more negative than values in normal subjects ($P <$

0.001). (Note the difference in scale in Figure 28A and Figure 28B). Amiloride inhibited V_t , as it did in normal subjects. However, V_t failed to hyperpolarize when terbutaline was perfused onto the epithelium in the presence of amiloride. Instead, V_t either did not change or became less negative: on average V_t depolarized by $+1.8 \pm 0.6$ mV, a result very different from that observed in normal subjects. ($P < 0.001$).

After Ad2/CFTR-1 was applied, basal V_t became less negative in all three CF patients: Figure 29A shows an example from the third patient before (Figure 29A) and after (Figure 29B) treatment and Figures 30A, 30C, and 30E show the time course of changes in basal V_t for all three patients. The decrease in basal V_t suggests that application of Ad2/CFTR-1 corrected the CF electrolyte transport defect in nasal epithelium of all three patients. Additional evidence came from an examination of the response to terbutaline. Figure 30B shows that in contrast to the response before Ad2/CFTR-1 was applied, after virus replication, in the presence of amiloride, terbutaline stimulated V_t . Figures 30B, 30D, and 30F show the time course of the response. These data indicate that Ad2/CFTR-1 corrected the CF defect in Cl^- transport. Correction of the Cl^- transport defect cannot be attributed to the anesthesia/application procedure because it did not occur in patients treated with saline instead of Ad2/CFTR-1 (Figure 31). Moreover, the effects of the anesthesia were generalized on the nasal mucosa, but basal V_t decreased only in the area of virus administration. Finally, similar changes were observed in the left nasal mucosa of the third patient (Figures 30E and 30F), which had no symptomatic or physical response after the modified application procedure.

Unsuccessful attempts were made to detect CFTR transcripts by reverse transcriptase-PCR and by immunocytochemistry in cells from nasal brushings and biopsies. Although similar studies in animals have been successful (Zabner, J. et al. (1993) *Nature Gen.* (in press)), those studies used much higher doses of Ad2/CFTR-1. The lack of success in the present case likely reflects the small amount of available tissue, the low MOI, the fact that only a fraction of cells may have been corrected, and the fact that Ad2/CFTR-1 contains a low to moderate strength promoter (E1a) which produces much less mRNA and protein than comparable constructs using a much stronger CMV promoter (unpublished observation). The E1a promoter was chosen because CFTR normally expressed at very low levels in airway epithelial cells (Trapnell, B.C. et al. (1991) *Proc. Natl. Acad. Sci. USA* 88:6565-6569). It is also difficult to detect CFTR protein and mRNA in normal human airway epithelia, although function is readily detected because a single ion channel can conduct a very large number of ions per second and thus efficiently support Cl^- transport.

With time, the electrical changes that indicate correction of the CF defect reverted toward pretreatment values. However, the basal V_t appeared to revert more slowly than did the change in V_t produced by terbutaline. The significance of this difference is unknown, but it may reflect the relative sensitivity of the two measurements to expression of normal CFTR. In any case, this study was not designed to test the duration of correction because the treated

area was removed by biopsy on one side and the nasal mucosa on the other side was brushed to obtain cells for analysis at 7 to 10 days after virus administration, and then at approximately weekly intervals. Brushing the mucosa removes cells, disrupts the epithelium, and reduces basal V_t to zero for at least two days afterwards, thus preventing an accurate
5 assessment of duration of the effect of Ad2/CFTR-1.

Efficacy of adenovirus-mediated gene transfer.

The major conclusion of this study is that *in vivo* application of a recombinant adenovirus encoding CFTR can correct the defect in airway epithelial Cl^- transport that is
10 characteristic of CF epithelia.

Complementation of the Cl^- channel defect in human nasal epithelium could be measured as a change in basal voltage and as a change in the response to cAMP agonists. Although the protocol was not designed to establish duration, changes in these parameters were detected for at least three weeks. These results represent the first report that
15 administration of a recombinant adenovirus to humans can correct a genetic lesion as measured by a functional assay. This study contrasts with most earlier attempts at gene transfer to humans, in that a recombinant viral vector was administered directly to humans, rather than using a *in vitro* protocol involving removal of cells from the patient, transduction of the cells in culture, followed by reintroduction of the cells into the patient.

Evidence that the CF Cl^- transport defect was corrected at all three doses of virus, corresponding to 1, 3, and 25 MOI, was obtained. This result is consistent with earlier studies showing that similar MOIs reversed the CF fluid and electrolyte transport defects in primary cultures of CF airway cells grown as epithelia on permeable filter supports (Rich, D.P. et al. (1993) *Human Gene Therapy* 4:461-476 and Zabner et al. submitted for
20 publication): at an MOI of less than 1, cAMP-stimulated Cl^- secretion was partially restored, and after treatment with 1 MOI Ad2/CFTR-1 cAMP agonists stimulated fluid secretion that was within the range observed in epithelia from normal subjects. At an MOI of 1, a related adenovirus vector produced β -galactosidase activity in 20% of infected epithelial cells as assessed by fluorescence-activated cell analysis (Zabner et al. submitted for publication).
25 Such data would imply that pharmacologic dose of adenovirus in CF airways might correspond to an MOI of one. If it is estimated that there are 2×10^6 cells/cm² in the airway (Mariassy, A.T. in *Comparative Biology of the Normal Lung* (CRC Press, Boca Raton 1992), and that the airways from the trachea to the respiratory bronchioles have a surface area of 1400 cm² (Weibel, E.R. *Morphometry of the Human Lung* (Springer Verlag, Heidelberg,
30 1963) then there would be approximately 3×10^9 potential target cells. Assuming a particle to IU ratio of 100, this would correspond to approximately 3×10^{11} particles of adenovirus with a mass of approximately 75 μg . While obviously only a crude estimate, such information is useful in designing animal experiments to establish the likely safety profile of a human dose.

It is possible that an efficacious MOI of recombinant adenovirus could be less than the lowest MOI tested here. Some evidence suggests that not all cells in an epithelial monolayer need to express CFTR to correct the CF electrolyte transport defects. Mixing experiments showed that when perhaps 5-10% of cells overexpress CFTR, the monolayer exhibits wild-type electrical properties (Johnson, L.G. et al. (1992) *Nature Gen.* 2:21-25). Studies using liposomes to express CFTR in mice bearing a disrupted CFTR gene also suggest that only a small proportion of cells need to be corrected (Hyde, S.C. et al. (1993) *Nature* 362:250-255). The results referred to above using airway epithelial monolayers and multiplicities of Ad2/CFTR-1 as low as 0.1 showed measurable changes in Cl^- secretion (Rich, D.P. et al. (1993) *Human Gene Therapy* 4:461-476 and Zabner et al. submitted for publication).

Given the very high sensitivity of electrolyte transport assays (which result because a single Cl^- channel is capable of transporting large numbers of ions/sec) and the low activity of the E1a promoter used to transcribe CFTR, the inability to detect CFTR protein and CFTR mRNA are perhaps not surprising. Although CFTR mRNA could not be detected by reverse transcriptase-PCR, Ad2/CFTR-1 DNA could be detected in the samples by standard PCR, demonstrating the presence of input DNA and suggesting that the reverse transcriptase reaction may have been suboptimal. This could have occurred because of factors in the tissue that inhibit the reverse transcriptase. Although there is little doubt that the changes in electrolyte transport measured here result from expression of CFTR, it remains to be seen whether this will lead to measurable clinical changes in lung function.

Safety considerations.

Application of the adenovirus vector to the nasal epithelium in these three patients was well-tolerated. Although mild inflammation was observed in the nasal epithelium of all three patients following administration of Ad2/CFTR-1, similar changes were observed in two volunteers who underwent a sham procedure using saline rather than the viral vector. Clearly a combination of anesthetic- and procedure-related trauma resulted in the changes in the nasal mucosa. There is insufficient evidence to conclude that no inflammation results from virus administration. However, using a modified administration of the highest MOI of virus tested (25 MOI) in one patient, no inflammation was observed under conditions that resulted in evidence of biophysical efficacy that lasted until the area was removed by biopsy at three days.

There was no evidence of replication of Ad2/CFTR-1. Earlier studies had established that replication of Ad2/CFTR-1 in tissue culture and experimental animals is severely impaired (Rich, D.P. et al. (1993) *Human Gene Therapy* 4:461-476; Zabner, J. et al. (1993) *Nature Gen.* (in press)). Replication only occurs in cells that supply the missing early proteins of the E1 region of adenovirus, such as 293 cells, or under conditions where the E1 region is provided by coinfection with or recombination with an E1-containing adenovirus

(Graham, F.L. and Prevec, L. Vaccines: New Approaches to Immunological Problems (R.W. Ellis, ed., Boston, Butterworth-Heinemann, 1992); Berkner, K.L. (1988) *Biotechniques* 6:616-629). The patients studied here were seropositive for adenovirus types 2 and 5 prior to the study were negative for adenovirus upon culture of nasal swabs prior to administration of Ad2/CFTR-1, and were shown by PCR methods to lack endogenous E1 DNA sequences such as have been reported in some human subjects (Matsuse T. et al. (1992) *Am. Rev. Respir. Dis.* 146:177-184).

Example 11 - Construction and Packaging of Pseudo Adenoviral Vector (PAV)

With reference to Figure 32, the PAV construct was made by inserting the Ad2 packaging signal and E1 enhancer region (0-358 nt) in Bluescript II SK- (Stratagene, LaJolla, CA). A variation of this vector, known as PAV II was constructed similarly, except the Ad2 packaging signal and E1 enhancer region contained 0-380 nt. The addition of nucleotides at the 5' end results in larger PAVs, which may be more efficiently packaged, yet would include more adenoviral sequences and therefore could potentially be more immunogenic or more capable of replicating.

To allow ease of manipulation for either the insertion of gene coding regions or complete excision and use in transfections for the purpose of generating infectious particles, a complementary plasmid was also built in pBluescript SKII-. This complementary plasmid contains the Ad2 major late promoter (MLP) and tripartite leader (TPL) DNA and an SV40 T-antigen nuclear localization signal (NLS) and polyadenylation signal (SVpA). As can be seen in Figure 32, this plasmid contains a convenient restriction site for the insertion of genes of interest between the MLP/TPL and SV40 poly A. This construct is engineered such that the entire cassette may be excised and inserted into the former PAV I or PAV II construct.

Generation of PAV infectious particles was performed by excision of PAV from the plasmid with the Apa I and Sac II restriction endonucleases and co-transfection into 293 cells (an Ela/Elb expressing cell line) (Graham, F.L. et al, (1977) *J. Gen Virol* 36:59-74) with either wild-type Ad2, or packaging/replication deficient helper virus. Purification of PAV from helper can be accompanied by CsCl gradient isolation as PAV viral particles will be of a lower density and will band at a higher position in the gradient.

For gene therapy, it is desirable to generate significant quantities of PAV virion free from contaminating helper virus. The primary advantage of PAV over standard adenoviral vectors is the ability to package large DNA inserts into virion (up to about 36 kb). However, PAV requires a helper virus for replication and packaging and this helper virus will be the predominant species in any PAV preparation. To increase the proportion of PAV in viral preparation several approaches can be employed. For example, one can use a helper virus which is partially defective for packaging into virions (either by virtue of mutations in the packaging sequences (Grable, M. and Hearing P. (1992) *J. Virol.* 66: 723-731)) or by virtue of its size -viruses with genome sizes greater than approximately 37.5 kb package

inefficiently. In mixed infections with packaging defective virus, PAV would be expected to be represented at higher levels in the virus mixture than would occur with non-packaging defective helper viruses.

Another approach is to make the helper virus dependent upon PAV for its own replication. This may most easily be accomplished by deleting an essential gene from the helper virus (e.g. IX or a terminal protein) and placing that gene in the PAV vector. In this way neither PAV nor the helper virus is capable of independent replication - PAV and the helper virus are therefore co-dependent. This should result in higher PAV representation in the resulting virus preparation.

A third approach is to develop a novel packaging cell line, which is capable of generating significant quantities of PAV virion free from contaminating helper virus. A novel protein IX, (pIX) packaging system has been developed. This system exploits several documented features of adenovirus molecular biology. The first is that adenoviral defective particles are known to comprise up to 30% or more of standard wild-type adenoviral preparations. These defective or incomplete particles are stable and contain 15-95% of the adenoviral genome, typically 15-30%. Packaging of a PAV genome (15-30% of wild-type genome) should package comparably. Secondly, stable packaging of full-length Ad genome but not genomes <95% required the presence of the adenoviral gene designated pIX.

The novel packaging system is based on the generation of an Ad protein pIX expressing 293 cell line. In addition, an adenoviral helper virus engineered such that the E1 region is deleted but enough exogenous material is inserted to equal or slightly exceed the full length 36 kb size. Both of these two constructs would be introduced into the 293/pIX cell line as purified DNA. In the presence of pIX, yields of both predicted progeny viruses as seen in current PAV/Ad2 production experiments can be obtained. Virus containing lysates from these cells can then be titered independently (for the marker gene activity specific to either vector) and used to infect standard 293 (lacking pIX) at a multiplicity of infection of 1 relative to PAV. Since research with this line as well as from incomplete or defective particle research indicates that full length genomes have a competitive packaging advantage, it is expected that infection with an MOI of 1 relative to PAV will necessarily equate to an effective MOI for helper of greater than 1. All cells will presumably contain both PAV (at least 1) and helper (greater than 1). Replication and viral capsid production in this cell should occur normally but only PAV genomes should be packaged. Harvesting these 293/pIX cultures is expected to yield essentially helper-free PAV.

Example 12 - Construction of Ad2-E4/ORF 6

Ad2-E4/ORF6 (Figure 33 shows the plasmid construction of Ad2-E4/ORF6) which is an adenovirus 2 based vector deleted for all Ad2 sequences between nucleotides 32815 and 35577. This deletion removes all open reading frames of E4 but leaves the E4 promoter and first 32-37 nucleotides of the E4 mRNA intact. In place of the deleted sequences, a DNA

fragment encoding ORF6 (Ad2 nucleotides 34082-33178) which was derived by polymerase chain reaction of Ad2 DNA with ORF6 specific DNA primers (Genzyme oligo. # 2371 - CGGATCCTTTATTATAGGGGAAGTCCACGCCTAC (SEQ. ID NO:8) and oligo. #2372 - CGGGATCCATCGATGAAATATGACTACGTCCG (SEQ. ID NO:9) were inserted). Additional sequences supplied by the oligonucleotides included a cloning site at the 5' and 3' ends of the PCR fragment (Clal and BamHI respectively) and a polyadenylation sequence at the 3' end to ensure correct polyadenylation of the ORF6 mRNA. As illustrated in Figure 33, the PCR fragment was first ligated to a DNA fragment including the inverted terminal repeat (ITR) and E4 promoter region of Ad2 (Ad2 nucleotides 35937-35577) and cloned in the bacterial plasmid pBluescript (Stratagene) to create plasmid ORF6. After sequencing to verify the integrity of the ORF6 reading frame, the fragment encompassing the ITR and ORF6 was subcloned into a second plasmid, pAd Δ E4, which contains the 3' end of Ad2 from a Sac I site to the 3' ITR (Ad2 nucleotides 28562-35937) and is deleted for all E4 sequences (promoter to poly A site Ad2 positions 32815-35641) using flanking restriction sites. In this second plasmid, virus expressing only E4 ORF6, pAdORF6 was cut with restriction enzyme PacI and ligated to Ad2 DNA digested with PacI. This PacI site corresponds to Ad2 nucleotide 28612. 293 cells were transfected with the ligation and the resulting virus was subjected to restriction analysis to verify that the Ad2 E4 region had been substituted with the corresponding region of pAdORF6 and that the only remaining E4 open reading frame was ORF6.

A cell line could in theory be established that would fully complement E4 functions deleted from a recombinant virus. The problem with this approach is that E4 functions in the regulation of host cell protein synthesis and is therefore toxic to cells. The present recombinant adenoviruses are deleted for the E1 region and must be grown in 293 cells which complement E1 functions. The E4 promoter is activated by the Ela gene product, and therefore to prevent inadvertent toxic expression of E4 transcription of E4 must be tightly regulated. The requirements of such a promoter or transactivating system is that in the uninduced state expression must be low enough to avoid toxicity to the host cell, but in the induced state must be sufficiently activated to make enough E4 gene product to complement the E4 deleted virus during virus production.

Example 13

An adenoviral vector is prepared as described in Example 7 while substituting the phosphoglycerate kinase (PGK) promoter for the Ela promoter.

Example 14

An adenoviral vector is prepared as described in Example 11 while substituting the PGK promoter for the Ad2 major late promoter (MLP).

Example 15: Generation of Ad2-ORF6/PGK-CFTR

This protocol uses a second generation adenovirus vector named Ad2-ORF6/PGK-CFTR. This virus lacks E1 and in its place contains a modified transcription unit with the PGK promoter and a poly A addition site flanking the CFTR cDNA. The PGK promoter is of only moderate strength but is long lasting and not subject to shut off. The E4 region of the vector has also been modified in that the whole coding sequence has been removed and replaced by ORF6, the only E4 gene essential for growth of Ad in tissue culture. This has the effect of generating a genome of 101% the size of wild type Ad2.

The DNA construct comprises a full length copy of the Ad2 genome from which the early region 1 (E1) genes (present at the 5' end of the viral genome) have been deleted and replaced by an expression cassette encoding CFTR. The expression cassette includes the promoter for phosphoglycerate kinase (PGK) and a polyadenylation (poly A) addition signal from the bovine growth hormone gene (BGH). In addition, the E4 region of Ad2 has been deleted and replaced with only open reading frame 6 (ORF6) of the Ad2 E4 region. The adenovirus vector is referred to as AD2-ORF6/PGK-CFTR and is illustrated schematically in Figure 34. The entire wild-type Ad2 genome has been previously sequenced (Roberts, R.J., (1986) In Adenovirus DNA, W. Oberfler, editor, Martinus Nihoff Publishing, Boston) and the existing numbering system has been adopted here when referring to the wild type genome. Ad2 genomic regions flanking E1 and E4 deletions, and insertions into the genome are being completely sequenced.

The Ad2-ORF6/PGK-CFTR construct differs from the one used in our earlier protocol (Ad2/CFTR-1) in that the latter utilized the endogenous E1a promoter, had no poly A addition signal directly downstream of CFTR and retained an intact E4 region. The properties of Ad2/CFTR-1 in tissue culture and in animal studies have been reported (Rich et al., (1993) *Human Gene Therapy* 4:461-467; and Zabner et al. (1993) *Nature Genetics* (in Press)).

At the 5' end of the genome, nucleotides 357 to 3328 of Ad2 have been deleted and replaced with (in order 5' to 3') 22 nucleotides of linker, 534 nucleotides of the PGK promoter, 86 nucleotides of linker, nucleotides 123-4622 of the published CFTR sequence (Riordan et al. (1989) *Science* 245:1066-1073), 21 nucleotides of linker, and a 32 nucleotide synthetic BGH poly A addition signal followed by a final 11 nucleotides of linker. The topology of the 5' end of the recombinant molecule is illustrated in Figure 34.

At the 3' end of the genome of Ad2-ORF6/PGK-CFTR, Ad2 sequences between nucleotides 32815 and 35577 have been deleted to remove all open reading frames of E4 but retain the E4 promoter, the E4 cap sites and first 32-37 nucleotides of E4 mRNA. The deleted sequences were replaced with a fragment derived by PCR which contains open reading frame 6 of Ad2 (nucleotides 34082-33178) and a synthetic poly A addition signal. The topology of the 3' end of the molecule is shown in Figure 34. The sequence of this segment of the molecule will be confirmed. The remainder of the Ad2 viral DNA sequence is

published in Roberts, R.J. in Adenovirus DNA. (W. Oberfler, Martinus Nihoff Publishing, Boston, 1986). The overall size of the Ad2-ORF6/PGK-CFTR vector is 36,336 bp which is 101.3% of full length Ad2. See Table III for the sequence of Ad2-ORF6/PGK-CFTR.

The CFTR transcript is predicted to initiate at one of three closely spaced
5 transcriptional start sites in the cloned PGK promoter (Singer-Sam et al. (1984) *Gene* 32:409-417) at nucleotides 828, 829 and 837 of the recombinant vector (Singer-Sam et al. (1984) *Gene* 32:409-417). A hybrid 5' untranslated region is comprised of 72, 80 or 81 nucleotides of PGK promoter region, 86 nucleotide of linker sequence, and 10 nucleotides derived from the CFTR insert. Transcriptional termination is expected to be directed by the BGH poly A
10 addition signal at recombinant vector nucleotide 5530 yielding an approximately 4.7 kb transcript. The CFTR coding region comprises nucleotides 1010-5454 of the recombinant virus and nucleotides 182, 181 or 173 to 4624, 4623, or 4615 of the PGK-CFTR-BGH mRNA respectively, depending on which transcriptional initiation site is used. Within the CFTR cDNA there are two differences from the published (Riordan et al, *cited supra*) cDNA
15 sequence. An A to C change at position 1990 of the CFTR cDNA (published CFTR cDNA coordinates) which was an error in the original published sequence, and a T to C change introduced at position 936. The change at position 936 is translationally silent but increases the stability of the cDNA when propagated in bacterial plasmids (Gregory et al. (1990) *Nature* 347:382-386; and Cheng et al. (1990) *Cell* 63:827-834). The 3' untranslated region of
20 the predicted CFTR transcript comprises 21 nucleotides of linker sequence and approximately 10 nucleotides of synthetic BGH poly A additional signal.

Although the activity of CFTR can be measured by electrophysiological methods, it is relatively difficult to detect biochemically or immunocytochemically, particularly at low levels of expression (Gregory et al., *cited supra*; and Denning et al. (1992) *J. Cell Biol.*
25 118:551-559). A high expression level reporter gene encoding the *E. coli* β galactosidase protein fused to a nuclear localization signal derived from the SV40 T-antigen was therefore constructed. Reporter gene transcription is driven by the powerful CMV early gene constitutive promoter. Specifically, the E1 region of wild type Ad2 between nucleotides 357-3498 has been deleted and replaced it with a 515 bp fragment containing the CMV promoter
30 and a 3252 bp fragment encoding the β galactosidase gene.

Regulatory Characteristics of the Elements of the AD2-ORF6/PGK-CFTR

In general terms, the vector is similar to several earlier adenovirus vectors encoding CFTR but it differs in three specific ways from the Ad2/CFTR-1 construct.

35

PGK Promoter

Transcription of CFTR is from the PGK promoter. This is a promoter of only moderate strength but because it is a so-called house keeping promoter we considered it more likely to be capable of long term albeit perhaps low level expression. It may also be less

likely to be subject to "shut-down" than some of the very strong promoters used in other studies especially with retroviruses. Since CFTR is not an abundant protein longevity of expression is probably more critical than high level expression. Expression from the PGK promoter in a retrovirus vector has been shown to be long lasting (Apperley et al. (1991) *Blood* 78:310-317).

Polyadenylation Signal

Ad2-ORG6/PGK-CFTR contains an exogenous poly A addition signal after the CFTR coding region and prior to the protein IX coding sequence of the Ad2 E1 region. Since protein is believed to be involved in packaging of virions, this coding region was retained. Furthermore, since protein IX is synthesized from a separate transcript with its own promoter, to prevent possible promoter occlusion at the protein IX promoter, the BGH poly A addition signal was inserted. There is indirect evidence that promoter occlusion can be problematic in that Ad2/CMV β Gal grows to lower viral titers on 293 cells than does Ad2/ β gal-1. These constructs are identical except for the promoter used for β galactosidase expression. Since the CMV promoter is much stronger than the E1a promoter it is probable that abundant transcription from the CMV promoter through the β galactosidase DNA into the protein IX coding region reduces expression of protein IX from its own promoter by promoter occlusion and that this is responsible for the lower titer of Ad2/CMV- β gal obtained.

Alterations of the E4 Region

A large portion of the E4 region of the Ad2 genome has been deleted for two reasons. The first reason is to decrease the size of the vector used or expression of CFTR. Adenovirus vectors with genomes much larger than wild type are packaged less efficiently and are therefore difficult to grow to high titer. The combination of the deletions in the E1 and E4 regions in Ad2-ORG6/PGK-CFTR reduce the genome size to 101% of wild type. In practice it is straightforward to prepare high titer lots of this virus.

The second reason to remove E4 sequences relates to the safety of adenovirus vectors. A goal of these studies is to remove as many viral genes as possible to inactivate the Ad2 virus backbone in as many ways as possible. The OF 6/7 gene of the E4 region encodes a protein that is involved in activation of the cellular transcription factor E2-F which is in turn implicated in the activation of the E2 region of adenovirus (Hemstrom et al. (1991) *J. Virol.* 65:1440-1449). Therefore removal of ORF6/7 from adenovirus vectors may provide a further margin of safety at least when grown in non-proliferating cells. The removal of the E1 region already renders such vectors disabled, in part because E1a, if present, is able to displace E2-F from the retinoblastoma gene product, thereby also contributing to the stimulation of E2 transcription. The ORF6 reading frame of Ad2 was added back to the E1-E4 backbone of the Ad2-ORG6/PGK-CFTR vector because ORF6 function is essential for production of the recombinant virus in 293 cells. ORF6 is believed to be involved in DNA replication, host

cell shut off and late mRNA accumulation in the normal adenovirus life cycle. The E1-E4-ORF6⁺ backbone Ad2 vector does replicate in 293 cells.

The promoter/enhancer use to drive transcription of ORF6 of E4 is the endogenous E4 promoter. This promoter requires E1a for activation and contains E1a core enhancer
5 elements and SP1 transcription factor binding sites (reviewed in Berk, A.J. (1986) *Ann. Rev. Genet.* 20:75-79).

Replication Origin

The only replication origins present in Ad2-ORF6/PGK-CFTR are those present in
10 the Ad2 parent genome. Replication of Ad2-ORF6/PGK-CFTR sequences has not been detected except when complemented with wild type E1 activity.

Steps Used to Derive the DNA Construct

Construction of the recombinant Ad2-ORF6/PGK-CFTR virus was accomplished by
15 *in vivo* recombination of Ad2-ORF6 DNA and a plasmid containing the 5' 10.7 kb of adenovirus engineered to have an expression cassette encoding the human CFTR cDNA driven by the PGK promoter and a BGH poly A signal in place of the E1 coding region.

The generation of the plasmid, pBRAd2/PGK-CFTR is described here. The starting plasmid contains an approximately 7.5 kb insert cloned into the ClaI and BamHI sites of
20 pBR322 and comprises the first 10,680 nucleotides of Ad2 with a deletion of the Ad2 sequences between nucleotides 356 and 3328. This plasmid contains a CMV promoter inserted into the ClaI and SpeI sites at the region of the E1 deletion and is designated pBRAd2/CMV. The plasmid also contains the Ad2 5' ITR, packaging and replication sequences and E1 enhancer. The E1 promoter, E1a and most of E1b coding region has been
25 deleted. The 3' terminal portion of the E1b coding region coincides with the pIX promoter which was retained. The CMV promoter was removed and replaced with the PGK promoter as a ClaI and SpeI fragment from the plasmid PGK-GCR. The resulting plasmid, pBRAd2/PGK, was digested with AvrII and BstBI and the excised fragment replaced with the SpeI to BstBI fragment from the plasmid construct pAd2E1a/CFTR. This transferred a
30 fragment containing the CFTR cDNA, BGH poly A signal and the Ad2 genomic sequences from 3327 to 10,670. The resulting plasmid is designated pBRAd2/PGK-CFTR. The CFTR cDNA fragment was originally derived from the plasmid pCMV-CFTR-936C using restriction enzymes SpeI and Ecl136II. pCMV-CFTR-936C consists of a minimal CFTR cDNA encompassing nucleotides 123-4622 of the published CFTR sequence cloned into the
35 multiple cloning site of pRC/CMV (Invitrogen Corp.) using synthetic linkers. The CFTR cDNA within this plasmid has been completely sequenced.

The Ad2 backbone virus with the E4 region that expresses only open reading frame 6 was constructed as follows. A DNA fragment encoding ORF6 (Ad2 nucleotides 34082-33178) was derived by PCR with ORF6 specific DNA primers. Additional sequences

supplied by the oligonucleotides include cloning sites at the 5' and 3' ends of the PCR fragment. (ClaI and BamHI respectively) and a poly A addition sequence AATAAA at the 3' end to ensure correct polyadenylation of ORF6 mRNA. The PCR fragment was cloned into pBluescript (Stratagene) along with an Ad2 fragment (nucleotides 35937-35577) containing the inverted terminal repeat, E4 promoter, E4 mRNA cap sites and first 32-37 nucleotides of E4 mRNA to create pORF6. A Sall-BamHI fragment encompassing the ITR and ORF6 was used to replace the Sall-BamHI fragment encompassing the ITR and E4 deletion in pAdΔE4 contains the 3' end of Ad2 from a SpeI site to the 3' ITR (nucleotides 27123-35937) and is deleted for all E4 sequences including the promoter and poly A signal (nucleotides 32815-35641). The resulting construct, pAdE4ORF6 was cut with PacI and ligated to Ad2 DNA digested with PacI nucleotide 28612). 293 cells were transfected with the ligation reaction to generate virus containing only open reading frame 6 from the E4 region.

In Vitro Studies with Ad2-ORF6/PGK-CFTR

The ability of Ad2-ORF6/PGK-CFTR to express CFTR in several cell lines, including human HeLa cells, human 293 cells, and primary cultures of normal and CF human airway epithelia was tested. As an example, the results from the human 293 cells is related here. When human 293 cells were grown on culture dishes, the vector was able to transfer CFTR cDNA and express CFTR as assessed by immunoprecipitation and by functional assays of halide efflux. Gregory, R.J. et al. (1990) *Nature* 347:382-386; Cheng, S.H. et al. (1990) *Cell* 63:827-834. More specifically, procedures for preparing cell lysates, immunoprecipitation of proteins using anti-CFTR antibodies, one-dimensional peptide analysis and SDS-polyacrylamide gel electrophoresis were as described by Cheng et al. Cheng, S.H. et al. (1990) *Cell* 63:827-834. Halide efflux assays were performed as described by Cheng, S.H. et al. (1991) *Cell* 66:1027-1036. cAMP-stimulated CFTR chloride channel activity was measured using the halide sensitive fluorophore SPQ in 293 cells treated with 500 IU/cell Ad2-ORF6/PGK-CFTR. Stimulation of the infected cells with forskolin (20 μM) and IBMX (100 μM) increased SPQ fluorescence indicating the presence of functional chloride channels produced by the vector.

Additional studies using primary cultures of human airway (nasal polyp) epithelial cells (from CF patients) infected with Ad2-ORF6/PGK-CFTR demonstrated that Ad2-ORF6/PGK-CFTR infection of the nasal polyp epithelial cells resulted in the expression of cAMP dependent Cl⁻ channels. Figure 35 is an example of the results obtained from such studies. Primary cultures of CF nasal polyp epithelial cells were infected with Ad2-ORF6/PGK-CFTR at multiplicities of 0.3, 3, and 50. Three days post infection, monolayers were mounted in Ussing chambers and short-circuit current was measured. At the indicated times: (1) 10 μM amiloride, (2) cAMP agonists (10 μM forskolin and 100 μM IBMX), and (3) 1 mM diphenylamine-2-carboxylate were added to the mucosal solution.

In Vivo Studies with Ad2-ORF6/PGK-CFTRVirus preparation

Two preparations of Ad2-ORF6/PGK-CFTR virus were used in this study. Both were prepared at Genzyme Corporation, in a Research Laboratory. The preparations were purified on a CsCl gradient and then dialyzed against tris-buffered saline to remove the CsCl. The preparation for the first administration (lot #2) had a titer of 2×10^{10} IU/ml. The preparation for the second administration (lot #6) had a titer of 4×10^{10} IU/ml.

Animals

Three female Rhesus monkeys, *Macaca mulatta*, were used for this study. Monkey C (#20046) weighed 6.4 kg. Monkey D (#20047) weighed 6.25 kg. Monkey E (#20048) weighed 10 kg. The monkeys were housed in the University of Iowa at least 360 days before the start of the study. The animals were maintained with free access to food and water throughout the study. The animals were part of a safety study and efficacy study for a different viral vector (Ad2/CFTR-1) and they were exposed to 3 nasal viral instillation throughout the year. The previous instillation of Ad2/CFTR-1 was performed 116 days prior to the initiation of this study. All three Rhesus monkeys had an anti-adenoviral antibody response as detected by ELISA after each viral instillation. There are no known contaminants that are expected to interfere with the outcome of this study. Fluorescent lighting was controlled to automatically provide alternate light/dark cycles of approximately 12 hours each. The monkeys were housed in an isolation room in separate cages. Strict respiratory and body fluid isolation precautions were taken.

Virus administration

For application of the virus, the monkeys were anesthetized by intramuscular injection of ketamine (15 mg/kg). The entire epithelium of one nasal cavity in each monkey was used for this study. A foley catheter (size 10) was inserted through each nasal cavity into the pharynx, the balloon was inflated with a 2-3 ml of air, and then pulled anteriorly to obtain a tight occlusion at the posterior choana. The Ad2-ORF6/PGK-CFTR virus was then instilled slowly into the right nostril with the posterior balloon inflated. The viral solution remained in contact with the nasal mucosa for 30 min. The balloons were deflated, the catheters were removed, and the monkeys were allowed to recover from anesthesia.

On the first administration, the viral preparation had a titer of 2×10^{10} IU/ml and each monkey received approximately 0.3 ml. Thus the total dose applied to each monkey was approximately 6.5×10^9 IU. This total dose is approximately half the highest dose proposed for the human study. When considered on a IU/kg basis, a 6 kg monkey received a dose approximately 3 times greater than the highest proposed dose for a 60 kg human.

Timing of evaluations.

The animals were evaluated on the day of administration, and on days 3, 7, 24, 38, and 44 days after infection. The second administration of virus occurred on day 44. The monkeys were evaluated on day 48 and then on days 55, 62, and 129.

- 5 For evaluations, monkeys were anesthetized by intramuscular injection of ketamine (15 mg/kg). To obtain nasal epithelial cells after the first viral administration, the nasal mucosa was first impregnated with 5 drops of Afrin (0.05% oxymetazoline hydrochloride, Schering-Plough) and 1 ml of 2% Lidocaine for 5 minutes. A cytobrush was then used to gently rub the mucosa for about 3 sec. To obtain pharyngeal epithelial swabs, a cotton-tipped applicator was rubbed over the back of the pharynx 2-3 times. The resulting cells were dislodged from brushes or applicators into 2 ml of sterile PBS. After the second administration of Ad2-ORF6/PGK-CFTR, the monkeys were followed clinically for 3 weeks, and mucosal biopsies were obtained from the monkeys medial turbinate at days 4, 11 and 18.

15 Animal evaluation.

Animals were evaluated daily for evidence of abnormal behavior or physical signs. A record of food and fluid intake was used to assess appetite and general health. Stool consistency was also recorded to check for the possibility of diarrhea. At each of the evaluation time points, rectal temperature, respiratory rate, and heart rate were measured. The nasal mucosa, conjunctivas and pharynx were visually inspected. The monkeys were also examined for lymphadenopathy.

Hematology and serum chemistry

- Venous blood from the monkeys was collected by standard venipuncture technique. Blood/serum analysis was performed in the clinical laboratory of the University of Iowa Hospitals and Clinics using a Hitachi 737 automated chemistry analyzer and a Technicom H6 automated hematology analyzer.

Serology

- 30 Sera from the monkeys were obtained and anti-adenoviral antibody titers were measured by ELISA. For the ELISA, 50 ng/well of killed adenovirus (Lee Biomolecular Research Laboratories, San Diego, Ca) was coated in 0.1M NaHCO₃ at 4° C overnight on 96 well plates. The test samples at appropriate dilutions were added, starting at a dilution of 1/50. The samples were incubated for 1 hour, the plates washed, and a goat anti-human IgG HRP conjugate (Jackson ImmunoResearch Laboratories, West Grove, PA) was added for 1 hour. The plates were washed and O-Phenylenediamine (OPD) (Sigma Chemical Co., St. Louis, MO) was added for 30 min. at room temperature. The assay was stopped with 4.5 M H₂SO₄ and read at 490 nm on a Molecular Devices microplate reader. The titer was calculated as the product of the reciprocal of the initial dilution and the reciprocal of the

dilution in the last well with an OD>0.100. Nasal washings from the monkeys were obtained and anti-adenoviral antibody titers were measured by ELISA, starting at a dilution of 1/4.

Nasal Washings.

- 5 Nasal washings were obtained to test for the possibility of secretory antibodies that could act as neutralizing antibodies. Three ml of sterile PBS was slowly instilled into the nasal cavity of the monkeys, the fluid was collected by gravity. The washings were centrifuged at 1000 RPM for 5 minutes and the supernatant was used for anti-adenoviral, and neutralizing antibody measurement.

10

Cytology

- Cells were obtained from the monkey's nasal epithelium by gently rubbing the nasal mucosa for about 3 seconds with a cytobrush. The resulting cells were dislodged from the brushes into 2 ml of PBS. The cell suspension was spun at 5000 rpm for 5 min. and
15 resuspended in 293 media at a concentration of 10^6 cells/ml. Forty μ l of the cell suspension was placed on slides using a Cytospin. Cytospin slides were stained with Wright's stain and analyzed for cell differential using light microscopy.

Culture for Ad2-ORF6/PFK-CFTR

- 20 To assess for the presence of infectious viral particles, the supernatant from the nasal brushings and pharyngeal swabs of the monkeys were used. Twenty-five μ l of the supernatant was added in duplicate to 293 cells. 293 cells were used at 50% confluence and were seeded in 96 well plates. 293 cells were incubated for 72 hours at 37°C, then fixed with a mixture of equal parts of methanol and acetone for 10 min and incubated with an FITC
25 label anti-adenovirus monoclonal antibodies (Chemicon, Light Diagnostics, Temecuca, Ca) for 30 min. Positive nuclear immunofluorescence was interpreted as positive culture.

Immunocytochemistry for the detection of CFTR.

- Cells were obtained by brushing. Eighty μ l of cell suspension were spun onto gelatin-coated slides. The slides were allowed to air dry, and then fixed with 4% paraformaldehyde.
30 The cells were permeabilized with 0.2 Triton-X (Pierce, Rockford, Il) and then blocked for 60 minutes with 5% goat serum (Sigma, Mo). A pool of monoclonal antibodies (M13-1, M1-4, and M6-4) (Gregory et al., (1990) *Nature* 347:382-386); Denning et al., (1992) *J. Cell Biol.* 118:(3) 551-559); Denning et al., (1992) *Nature* 358:761-764) were added and incubated for
35 12 hours. The primary antibody was washed off and an antimouse biotinylated antibody (Biomed, Foster City, Ca) was added. After washing, the secondary antibody, streptavidin FITC (Biomed, Foster City, Ca) was added and the slides were observed with a laser scanning confocal microscope.

Biopsies

To assess for histologic evidence of safety, nasal medial turbinate biopsies were obtained on day 4, 11 and 18 after the second viral administration as described before (Zabner et al (1993) Human Gene Therapy, in press). Nasal biopsies were fixed in 4% formaldehyde and H&E stained sections were reviewed.

RESULTS

Studies of efficacy.

To directly assess the presence of CFTR, cells obtained by brushing were plated onto slides by cytospin and stained with antibodies to CFTR. A positive reaction is clearly evident in cells exposed to Ad2-ORF6/PGK-CFTR. The cells were scored as positive by immunocytochemistry when evaluated by a reader blinded to the identity of the samples. Cells obtained prior to infection and from other untreated monkeys were used as negative controls. Figures 36A-36D, 37A-37D, and 38A-38D show examples from each monkey.

Studies of safety

None of the monkeys developed any clinical signs of viral infections or inflammation. There were no visible abnormalities at days 3, 4, 7 or on weekly inspection thereafter. Physical examination revealed no fever, lymphadenopathy, conjunctivitis, coryza, tachypnea, or tachycardia at any of the time points. There was no cough, sneezing or diarrhea. The monkeys had no fever. Appetites and weights were not affected by virus administration in either monkey. The data are summarized in Figures 39A-39C.

The presence of live virus was tested in the supernatant of cell suspensions from swabs and brushes from each nostril and the pharynx. Each supernatant was used to infect the virus-sensitive 293 cell line. Live virus was never detected at any of the time points. The rapid loss of live virus suggests that there was no viral replication.

The results of complete blood counts, sedimentation rate, and clinical chemistries are shown in Figure 40A-40C. There was no evidence of a systemic inflammatory response or other abnormalities of the clinical chemistries.

Epithelial inflammation was assessed by cytological examination of Wright-stained cells (cytospin) obtained from brushings of the nasal epithelium. The percentage of neutrophils and lymphocytes from the infected nostrils were compared to those of the control nostrils and values from four control monkeys. Wright stains of cells from nasal brushing were performed on each of the evaluation days. Neutrophils and lymphocytes accounted for less than 5% of total cells at all time points. The data are shown in Figure 41. The data indicate that administration of Ad2-ORF6/PGK-CFTR caused no change in the distribution or number of inflammatory cells at any of the time points following virus administration,

even during a second administration of the virus. The biopsy slides obtained after the second Ad2-ORF6/PGK-CFTR administration were reviewed by an independent pathologist, who found no evidence of inflammation or any other cytopathic effects. Figures 42 to 44 show an example from each monkey.

5 Figures 45A-45C shows that all three monkeys had developed antibody titers to adenovirus prior to the first infection with Ad2-ORF6/PGK-CFTR (Zabner et al. (1993) *Human Gene Therapy* (in press)). Antibody titers measured by ELISA rose within one week after the first and second administration and peaked at day 24. No anti-adenoviral antibodies were detected by ELISA or neutralizing assay in nasal washings of any of the monkeys.

10 These results combined with demonstrate the ability of a recombinant adenovirus encoding CFTR (Ad2-ORF6/PGK-CFTR) to express CFTR cDNA in the airway epithelium of monkeys. These monkeys have been followed clinically for 12 months after the first viral administration and no complications have been observed.

15 The results of the safety studies are encouraging. No evidence of viral replication was found; infectious viral particles were rapidly cleared. The other major consideration for safety of an adenovirus vector in the treatment of CF is the possibility of an inflammatory response. The data indicate that the virus generated an antibody response, but despite this, no evidence of a systemic or local inflammatory response was observed. The cells obtained by brushings and swabs were not altered by virus application. Since these Monkeys had been
20 previously exposed three times to Ad2/CFTR-1, these data suggest that at least five sequential exposures of airway epithelium to adenovirus does not cause a detrimental inflammatory response.

25 These data indicate that Ad2-ORF6/PGK-CFTR can effectively transfer CFTR cDNA to airway epithelium and direct the expression of CFTR. They also indicate that transfer and expression is safe in primates.

Equivalents

30 Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents of the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

TABLE I

<u>Mutant</u>	<u>CF</u>	<u>Exon</u>	<u>CFTR Domain</u>	<u>A</u>	<u>B</u>
Wild Type				-	+
R334W	Y	7	TM6	-	+
K464M	N	9	NBD1	-	+
Δ1507	Y	10	NBD1	-	+
ΔF508	Y	10	NBD1	-	+
F508R	N	10	NBD1	-	+
S549I	Y	11	NBD1	-	+
G551D	Y	11	NBD1	-	+
N894,900Q	N	15	ECD4	+	-
K1250M	N	20	NBD2	-	+
Tth111	N	22	NB-Term	-	+

Table II.

10	20	30	40	50	60
CATCATCAAT	AATATACCTT	ATTTTGGATT	GAAGCCAATA	TGATAATGAG	GGGGTGGAGT
GTAGTAGTTA	TTATATGGAA	TAAAACCTAA	CTTCGGTTAT	ACTATTACTC	CCCCACCTCA
_____INVERTED TERMINAL REPETITION-ORIGIN OF REPLICATION_____					60>
70	80	90	100	110	120
TTGTGACGTG	GCGCGGGGCG	TGGGAACGGG	GCGGGTGACG	TAGTAGTGTG	GCGGAAGTGT
AACACTGCAC	CGCGCCCCGC	ACCGTTGCCC	CGCCCACTGC	ATCATCACAC	CGCCTTCACA
_____INVERTED TERMINAL REPETITION-ORIGIN OF R_____>					
130	140	150	160	170	180
GATGTTGCAA	GTGTGGCGGA	ACACATGTAA	GCGCCGGATG	TGGTAAAAGT	GACGTTTTTG
CTACAACGTT	CACACCGCCT	TGTGTACATT	CGCGGCCTAC	ACCATTTTCA	CTGCAAAAAC
190	200	210	220	230	240
GTGTGCGCCG	GTGTATACGG	GAAGTGACAA	TTTTGCGCGG	GTTTtagGCG	GATGTTGTAG
CACACGCGGC	CACATATGCC	CTTCACGTGT	AAAAGCGCGC	CAAATCCGC	CTACAACATC
_____b_____E1A ENHANCER AND VIRAL PACKAGING DOMAIN_____					50>
250	260	270	280	290	300
TAAATTTGGG	CGTAACCAAG	TAATGTTTGG	CCATTTTCGC	GGGAAAAGTG	AATAAGAGGA
ATTTAAACCC	GCAATTGGTT	ATTACAAACC	GGTAAAAGCG	CCCTTTTGAC	TTATTCTCCT
_____60_b_____E1A ENHANCER AND VIRAL PACKAGING DOMAIN_____					110>
310	320	330	340	350	360
AGTGAAATCT	GAATAATTCT	GTGTTACTCA	TAGCGCGTAA	TATTTGTCTA	GGGCCGCGGG
TCACTTTAGA	CTTATTAAGA	CACAATGAGT	ATCGCGCATT	ATAAACAGAT	CCCGGCGCCC
_____120_b_____E1A ENHANCER AND VIRAL PACKAGING DOMAIN_____					170>
370	380	390	400	410	420
GACTTTGACC	GTTTACGTGG	AGACTCGCCC	AGSTGTTTTT	CTCAGGTGTT	TTCCGCGTTC
CTGAAACTGG	CAAATGCACC	TCTGAGCGGG	TCCACAAAAA	GAGTCCACAA	AAGGCGCAAG
_____E1A ENHANCER A_____90>					
_____c_____10_E1A PROMOTER REGION_____					40>
430	440	450	460	470	480
CGGGTCAAAG	TTGGCGTTTT	ATTATTATAG	TCAGCTGACG	CGCAGTGTAT	TTATACCCGG
GCCCACTTTC	AACCGCAAAA	TAAATATATC	AGTCGACTGC	GCGTCACATA	AATATGGGCC
_____50_c_____60_____E1A PROMOTER REGION_____					90_c_____100>
490	500	510	520	530	540
TGAGTTCCCTC	AAGAGGCCAC	TCTTGAGTGC	CAGCGAGTAG	AGTTTTCTCC	TCCGAGCCGC
ACTCAAGGAG	TTCTCCGGTG	AGAATCAGC	GTCGTCATC	TCAAAGAGAG	AGGCTCGGCG
_____h_____HYBRID E1A-CFTR-E1B MESSAGE_____>					
_____E1A PROMOTER_____120>					
_____i_____E1A mRNA 5' UNTRANSLATED_____					40>
550	560	570	580	590	600
TCCGAGCTAG	TAACGGCCGC	CAGTGTGCTG	CAGATATCAA	AGTCGACGGT	ACCCGAGAGA
AGGCTCGATC	ATTGCCGGCG	GTCACACGAC	GTCTATAGTT	TCAGGTGCCA	TGGGTCCTCT

_____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
____>
_____e_____10_____SYNTHETIC LINKER SEQUENCES_____40_____e_____>
_____130>

610 620 630 640 650 660
CCATGCAGAG GTGCGCTCTG GAAAAGGCCA GCGTTGTCTC CAAACTTTTT TTCAGCTGGA
GGTACGTCTC CAGCGGAGAC CTTTCCGGT CGCAACAGAG GTTTGAAAAA AAGTCGACCT
M Q R S P L E K A S V V S K L F F S W>
_____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; COD_____>
_____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
_____140i_____123 TO 4622 OF HUMAN CFTR CDNA_____180i_____190>

670 680 690 700 710 720
CCAGACCAAT TTTGAGGAAA GGATACAGAC AGCGCCTGGA ATTGTCAGAC ATATACCAA
GGTCTGGTTA AAACCTCCTT CCTATGTCTG TCGCGGACCT TAACAGTCTG TATATGGTTT
T R P I L R K G Y R Q R L E L S D I Y Q>
_____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON_____>
_____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
_____200i_____123 TO 4622 OF HUMAN CFTR CDNA_____240i_____250>

730 740 750 760 770 780
TCCCTTCTGT TGATTCTGCT GACAATCTAT CTGAAAAATT GGAAAGAGAA TGGGATAGAG
AGGGAAGACA ACTAAGACGA CTGTTAGATA GACTTTTAA CCTTTCTCTT ACCCTATCTC
I P S V D S A D N L S E K L E R E W D R>
_____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON_____>
_____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
_____260i_____123 TO 4622 OF HUMAN CFTR CDNA_____300i_____310>

790 800 810 820 830 840
AGCTGGCTTC AAAGAAAAAT CCTAACTCA TTAATGCCCT TCGGCGATGT TTTTCTGGA
TCGACCGAAG TTTCTTTTAA GGATTTGAGT AATTACGGGA AGCCGCTACA AAAAAGACCT
E L A S K K N P K L I N A L R R C F F W>
_____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON_____>
_____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
_____320i_____123 TO 4622 OF HUMAN CFTR CDNA_____360i_____370>

850 860 870 880 890 900
GATTTATGTT CTATGGAATC TTTTATATT TAGGGGAAGT CACCAAAGCA GTACAGCCTC
CTAAATACAA GATACCTTAG AAAATATATA ATCCCTTCA GTGGTTTCGT CATGTGGGAG
R F M F Y G I F L V L G E V T K A V Q P>
_____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON_____>
_____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
_____380i_____123 TO 4622 OF HUMAN CFTR CDNA_____420i_____430>

910 920 930 940 950 960
TCTTACTGGG AAGATCATA GCTTCCTATG ACCCGGATAA CAAGGAGGAA CGCTCTATCG
AGAATGACCC TTCTTAGTAT CGAAGGATAC TGGGCTTATT GTTCCTCCTT GCGAGATAGC
L L L G R I I A S Y D P D N K E E R S I>
_____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON_____>
_____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
_____440i_____123 TO 4622 OF HUMAN CFTR CDNA_____480i_____490>

970 980 990 1000 1010 1020
CGATTTATCT AGGCATAGGC TTATGCCCTC TCTTTATTGT GAGGACACTG CTCCTACACC

GCTAAATAGA TCCGTATCCG AATACGGAAG AGAAATAACA CTCCTGTGAC GAGGATGTGG
 A I Y L G I G L C L L F I V R T L L L H>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____>
 ____500i____123 TO 4622 OF HUMAN CFTR CDNA____540i____550>

1030

1040

1050

1060

1070

1080

CAGCCATTTT TGGCCTTCAT CACATTGGAA TGCAGATGAG AATAGCTATG TTTAGTTTGA
 GTCGGTAAAA ACCGGAAGTA GTGTAACCTT ACGTCTACTC TTATCGATAC AAATCAAAC
 P A I F G L H H I G M Q M R I A M F S L>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____>
 ____560i____123 TO 4622 OF HUMAN CFTR CDNA____600i____610>

1090

1100

1110

1120

1130

1140

TTTATAAGAA GACTTTAAAG CTGTCAAGCC GTGTTCTAGA TAAAATAAGT ATTGGACAAC
 AAATATTCTT CTGAAATTTC GACAGTTCGG CACAAGATCT ATTTTATTCA TAACCTGTTG
 I Y K K T L K L S S R V L D K I S I G Q>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____>
 ____620i____123 TO 4622 OF HUMAN CFTR CDNA____660i____670>

1150

1160

1170

1180

1190

1200

TTGTTAGTCT CCTTTCCAAC AACCTGAACA AATTTGATGA AGGACTTGCA TTGGCACATT
 AACATCAGA GGAAAGGTTG TTGGACTTGT TTAAACTACT TCCTGAACGT AACCGTGTA
 L V S L L S N N L N K F D E G L A L A H>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____>
 ____680i____123 TO 4622 OF HUMAN CFTR CDNA____720i____730>

1210

1220

1230

1240

1250

1260

TCGTGTGGAT CGCTCCTTTG CAAGTGGCAC TCCTCATGGG GCTAATCTGG GAGTTGTTAC
 AGCACACCTA GCGAGGAAAC GTTCACCGTG AGGAGTACCC CGATTAGACC CTCAACAATG
 F V W I A P L Q V A L L M G L I W E L L>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____>
 ____740i____123 TO 4622 OF HUMAN CFTR CDNA____780i____790>

1270

1280

1290

1300

1310

1320

AGGCGTCTGC CTTCTGTGGA CTTGGTTTCC TGATAGTCCT TGCCCTTTTT CAGGCTGGGC
 TCCGCAGACG GAAGACACCT GAACCAAAGG ACTATCAGGA ACGGGAFAAA GTCCGACCCG
 Q A S A F C G L G F L I V L A L F Q A G>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____>
 ____800i____123 TO 4622 OF HUMAN CFTR CDNA____840i____850>

1330

1340

1350

1360

1370

1380

TAGGGAGAAT GATGATGAAG TACAGAGATC AGAGAGCTGG GAAGATCACT GAAAGACTTG
 ATCCCTCTTA CTACTACTTC ATGTCTCTAG TCTCTCGACC CTTCTAGTCA CTTTCTGAAC
 L G R M M M K Y R D Q R A G K I S E R L>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____>
 ____860i____123 TO 4622 OF HUMAN CFTR CDNA____900i____910>

1390

1400

1410

1420

1430

1440

TGATTACCTC AGAAATGATT GAAAACATCC AATCTGTTAA GGCATACCTGC TGGGAAGAAG
 ACTAATGGAG TCTTTACTAA CTTTGTAGG TTAGACAATT CCGTATGACG ACCCTTCTTC
 V I T S E M I E N I Q S V K A Y C W E E
 _____ CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON _____>
 _____ h _____ HYBRID ELA-CFTR-ELB MESSAGE _____ h _____>
 _____ 920i _____ 123 TO 4622 OF HUMAN CFTR CDNA _____ 960i _____ 970>

1450 1460 1470 1480 1490 1500
 CAATGGAAAA AATGATTGAA AACTTAAGAC AACAGAACT GAAACTGACT CGGAAGGCAG
 GTTACCTTTT TTACTAAGTT TTGAATCTCG TTTGTCTTGA CTTTGACTGA GCCTTCCGTC
 A M E K M I E N L R Q T E L K L T R K A
 _____ CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON _____>
 _____ h _____ HYBRID ELA-CFTR-ELB MESSAGE _____ h _____>
 _____ 980i _____ 123 TO 4622 OF HUMAN CFTR CDNA _____ 1020i _____ 1030>

1510 1520 1530 1540 1550 1560
 CCTATGTGAG ATACTTCAAT AGCTCAGCCT TCTTCTTCTC AGGGTTCCTT GTGGTGTTTT
 GGATACACTC TATGAAGTTA TCGAGTCGGA AGAAGAAGAG TCCCAAGAAA CACCACAAAA
 A Y V R Y F N S S A F F F S G F F V V F
 _____ CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON _____>
 _____ h _____ HYBRID ELA-CFTR-ELB MESSAGE _____ h _____>
 _____ 1040i _____ 123 TO 4622 OF HUMAN CFTR CDNA _____ 1080i _____ 1090>

1570 1580 1590 1600 1610 1620
 TATCTGTGCT TCCCTATGCA CTAATCAAG GAATCATCCT CCGGAAAATA TTCACCA
 ATAGACACGA AGGGATACGT GATTAGTTTC CTTAGTAGGA GGCCTTTTAT AAGTGGTGGT
 L S V L P Y A L I K G I I L R K I F T T
 _____ CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON _____>
 _____ h _____ HYBRID ELA-CFTR-ELB MESSAGE _____ h _____>
 _____ 1100i _____ 123 TO 4622 OF HUMAN CFTR CDNA _____ 1140i _____ 1150>

1630 1640 1650 1660 1670 1680
 TCTCATTCTG CATTGTTCTG CGCATGGCGG TCACTCGGCA ATTTCCCTGG GCTGTACAAA
 AGAGTAAGAC GTAACAAGAC GCGTACCGCC AGTGAGCCGT TAAAGGGACC CGACATGTTT
 I S F C I V L R M A V T R Q F P W A V Q
 _____ CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON _____>
 _____ h _____ HYBRID ELA-CFTR-ELB MESSAGE _____ h _____>
 _____ 1160i _____ 123 TO 4622 OF HUMAN CFTR CDNA _____ 1200i _____ 1210>

1690 1700 1710 1720 1730 1740
 CATGSTATGA CTCTCTTGGA GCAATTAACA AATACAGGA TTTCTTACAA AAGCAAGAA
 GTACCATACT GAGAGAACCT CGTTATTTGT TTTATGTCCT AAAGAATGTT TTCGTTCTTA
 T W Y D S L G A I N K I Q D F L Q K Q E
 _____ CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON _____>
 _____ h _____ HYBRID ELA-CFTR-ELB MESSAGE _____ h _____>
 _____ 1220i _____ 123 TO 4622 OF HUMAN CFTR CDNA _____ 1260i _____ 1270>

1750 1760 1770 1780 1790 1800
 ATAAGACATT GGAATATAAC TTAACGACTA CAGAAGTAGT GATGGAGGAT GTAACAGCCT
 TATTCTGTAA CCTTATATTG AATTGCTGAT GTCTTCATCA CTACCTCTTA CATTGTCCGA
 Y K T L E Y N L T T T E V V M E N V T A
 _____ CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON _____>
 _____ h _____ HYBRID ELA-CFTR-ELB MESSAGE _____ h _____>
 _____ 1280i _____ 123 TO 4622 OF HUMAN CFTR CDNA _____ 1320i _____ 1330>

1810 1820 1830 1840 1850 1860

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TCTGGGAGGA GGGATTGTTGGG GAATTATTTG AGAAAGCAAA ACAAACAAT AACAATAGAA
 AGACCCTCCT CCCTAAACCC CTTAATAAC TCTTTCGTTT TGTTTTGTTA TTGTATCTT
 F W E E G F G E L F E K A K Q N N N N R>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____>
 ____1340i____123 TO 4622 OF HUMAN CFTR CDNA____1380i____1390>

1870 1880 1890 1900 1910 1920

AAACTTCTAA TGGTGATGAC AGCCTCTTCT TCAGTAATTT CTCACTTCTT GGTACTCCTG
 TTTGAAGATT ACCACTACTG TCGGAGAAGA AGTCATTAAA GAGTGAAGAA CCATGAGGAC
 K T S N G D D S L F F S N F S L L G T P>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____>
 ____1400i____123 TO 4622 OF HUMAN CFTR CDNA____1440i____1450>

1930 1940 1950 1960 1970 1980

TCCTGAAAGA TATTAATTTT AAGATAGAAA GAGGACAGTT GTTGGCGGTT GCTGGATCCA
 AGGACTTTCT ATAATTAAAG TTCTATCTTT CTCCTGTCAA CAACCGCCAA CGACCTAGGT
 V L K D I N F K I E R G Q L L A V A G S>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____>
 ____1460i____123 TO 4622 OF HUMAN CFTR CDNA____1500i____1510>

1990 2000 2010 2020 2030 2040

CTGGAGCAGG CAAGACTTCA CTTCTAATGA TGATTATGGG AGAACTGGAG CCTTCAGAGG
 GACCTCGTCC GTTCTGAAGT GAAGATTACT ACTAATACCC TCTTGACCTC GGAAGTCTCC
 T G A G K T S L L M M I M G E L E P S E>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____>
 ____1520i____123 TO 4622 OF HUMAN CFTR CDNA____1560i____1570>

2050 2060 2070 2080 2090 2100

GTAATATTAA GCACAGTGGG AGAATTTTCAT TCTGTTCTCA GTTTTCCTGG ATTATGCCTG
 CATTTTAATT CGTGTACCT TCTTAAAGTA AGACAAGAGT CAAAAGGACC TAATACGGAC
 G K I K H S G R I S F C S Q F S W I M P>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____>
 ____1580i____123 TO 4622 OF HUMAN CFTR CDNA____1620i____1630>

2110 2120 2130 2140 2150 2160

GCACCATTAAG AAAAATATC ATCTTTGGTG TTTCCTATGA TGAATATAGA TACAGAAGCG
 CGTGGAATTT TCTTTTATAG TAGAAACCAC AAAGGATACT ACTTATATCT ATGTCTTCGC
 G T I K E N I I F G V S Y D E Y R Y R S>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____>
 ____1640i____123 TO 4622 OF HUMAN CFTR CDNA____1680i____1690>

2170 2180 2190 2200 2210 2220

TCATCAAGC ATGCCAACTA GAAGAGGACA TCTCCAAGTT TGCAGAGAAA GACAATATAG
 AGTAGTTTCG TACGGTTGAT CTTCTCTGT AGAGGTTCAA ACGTCTCTTT CTGTTATATC
 V I K A C Q L E E D I S K F A E K D N I>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____>
 ____1700i____123 TO 4622 OF HUMAN CFTR CDNA____1740i____1750>

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2230	2240	2250	2260	2270	2280
TTCTTGGAGA AGGTGGAATC ACACTGAGTG GAGGTCAACG AGCAAGAATT TCCTTAGCAA AAGAACCTCT TCCACCTTAG TGTGACTCAC CTCCAGTTGC TCGTCTTAA AGAAATCGTT V L G E G G I T L S G G Q R A R I S L A> ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____> ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____> ____1760i____123 TO 4622 OF HUMAN CFTR CDNA____1800i____1810>					
2290	2300	2310	2320	2330	2340
GAGCAGTATA CAAAGATGCT GATTTGTATT TATTAGACTC TCCTTTTGGG TACCTAGATG CTCGTCATAT GTTCTACGA CTAAACATAA ATAATCTGAG AGGAAAACCT ATGGATCTAC R A V Y K D A D L Y L L D S P F G Y L D> ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____> ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____> ____1820i____123 TO 4622 OF HUMAN CFTR CDNA____1860i____1870>					
2350	2360	2370	2380	2390	2400
TTTTAACAGA AAAAGAAATA TTTGAAAGCT GTGTCTGTAA ACTGATGGCT AACAAACTA AAAATTGTCT TTTTCTTTAT AAACITTCGA CACAGACATT TGACTACCGA TTGTTTGTAT V L T E K E I F E S C V C K L M A N K T> ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____> ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____> ____1880i____123 TO 4622 OF HUMAN CFTR CDNA____1920i____1930>					
2410	2420	2430	2440	2450	2460
GGATTTTGGT CACTTCTAAA ATGGAACATT TAAAGAAAGC TGACAAAATA TTAATTTTGC CCTAAAACCA GTGAAGATTT TACCTTGTA AATTCTTTTCG ACTGTTTTAT AATTAAAACG R I L V T S K M E H L K K A D K I L I L> ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____> ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____> ____1940i____123 TO 4622 OF HUMAN CFTR CDNA____1980i____1990>					
2470	2480	2490	2500	2510	2520
ATGAAGGTAG CAGCTATTTT TATGGGACAT TTTCAGAACT CCAAATCTA CAGCCAGACT TACTTCCATC GTCGATAAAA ATACCCTGTA AAAGTCTTGA GGTTTTAGAT GTCGGTCTGA H E G S S Y F Y G T F S E L Q N L Q P D> ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____> ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____> ____2000i____123 TO 4622 OF HUMAN CFTR CDNA____2040i____2050>					
2530	2540	2550	2560	2570	2580
TTAGCTCAAA ACTCATGGA TGTGATTCTT TCGACCAATT TAGTGCAGAA AGAAGAAATT AATCGAGTTT TGASTACCCT AACTAAGAA AGCTGGTTAA ATCAGCTCTT TCTTCTTTAA F S S K L M G C D S F D Q F S A E R R N> ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____> ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____> ____2060i____123 TO 4622 OF HUMAN CFTR CDNA____2100i____2110>					
2590	2600	2610	2620	2630	2640
CAATCCTAAC TGAGACCTTA CACCGTTTCT CATTAGAAGG AGATGCTCCT GTCTCCTGGA GTTAGGATTG ACTCTGGAAT GTGGCAAGA GTAATCTTCC TCTACGAGGA CAGAGGACCT S I L T E T L H R F S L E G D A P V S W> ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____> ____h____HYBRID ELA-CFTR-ELB MESSAGE____h____> ____2120i____123 TO 4622 OF HUMAN CFTR CDNA____2160i____2170>					

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2650 2660 2670 2680 2690 2700
CAGAAACAAA AAAACAATCT TTAAACAGA CTGGAGAGTT TGGGGAAAAA AGGAAGAATT
GTCTTTGTTT TTTTGTTAGA AAATTTGTCT GACCTCTCAA ACCCCTTTT TCCTTCTTAA
T E T K K Q S F K Q T G E F G E K R K N>
____ CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
____ h____ HYBRID E1A-CFTR-E1B MESSAGE____ h____>
____ 2180i____ 123 TO 4622 OF HUMAN CFTR CDNA____ 2220i____ 2230>
2710 2720 2730 2740 2750 2760
CTATTCTCAA TCCAATCAAC TCTATACGAA AATTTTCCAT TGTGCAAAAG ACTCCCTTAC
GATAAGAGTT AGGTTAGTTG AGATATGCTT TTAAAAGGTA ACACGTTTTC TGAGGGAATG
S I L N P I N S I R K F S I V Q K T P L>
____ CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
____ h____ HYBRID E1A-CFTR-E1B MESSAGE____ h____>
____ 2240i____ 123 TO 4622 OF HUMAN CFTR CDNA____ 2280i____ 2290>
2770 2780 2790 2800 2810 2820
AAATGAATGG CATCGAAGAG GATTCTGATG AGCCTTTAGA GAGAAGGCTG TCCTTAGTAC
TTTACTTACC GTAGCTTCTC CTAAGACTAC TCGGAAATCT CTCTCCGAC AGGAATCATG
Q M N G I E E D S D E P L E R R L S L V>
____ CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
____ h____ HYBRID E1A-CFTR-E1B MESSAGE____ h____>
____ 2300i____ 123 TO 4622 OF HUMAN CFTR CDNA____ 2340i____ 2350>
2830 2840 2850 2860 2870 2880
CAGATTCTGA GCAGGGAGAG GCGATACTGC CTCGCATCAG CGTGATCAGC ACTGGCCCCA
GTCTAAGACT CGTCCCTCTC CGCTATGACG GAGCGTAGTC GCACTAGTCG TGACCGGGGT
P D S E Q G E A I L P R I S V I S T G P>
____ CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
____ h____ HYBRID E1A-CFTR-E1B MESSAGE____ h____>
____ 2360i____ 123 TO 4622 OF HUMAN CFTR CDNA____ 2400i____ 2410>
2890 2900 2910 2920 2930 2940
CGCTTCAGGC ACGAAGGAGG CAGTCTGTCC TGAACCTGAT GACACACTCA GTTAACCAAG
GCGAAGTCCG TGCTTCCTCC GTCAGACAGG ACTTGGACTA CTGTGTGAGT CAATTGGTTC
T L Q A R R R Q S V L N L M T H S V N Q>
____ CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
____ h____ HYBRID E1A-CFTR-E1B MESSAGE____ h____>
____ 2420i____ 123 TO 4622 OF HUMAN CFTR CDNA____ 2460i____ 2470>
2950 2960 2970 2980 2990 3000
GTCAGACAT TCACCGAAG ACAACAGCAT CCACACGAAA AGTGTCACTG GCCCCTCAGG
CACTCTTGTA AGTGGCTTTC TGTGTGCGTA GGTGTGCTTT TCACASTGAC CGGGGAGTCC
G Q N I H R K T T A S T R K V S L A P Q>
____ CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
____ h____ HYBRID E1A-CFTR-E1B MESSAGE____ h____>
____ 2480i____ 123 TO 4622 OF HUMAN CFTR CDNA____ 2520i____ 2530>
3010 3020 3030 3040 3050 3060
CAACTTGAC TGAAGTGGAT ATATATTCAA GAAGTTATC TCAAGAAACT GGCTTGGAAA
GTTTGAAGT ACTTGACCTA TATATACTT CTTCATAG AGTTCTTTGA CCGAACCTTT
A N L T E L D I Y S R R L S Q E T G L E>
____ CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
____ h____ HYBRID E1A-CFTR-E1B MESSAGE____ h____>

_____2540i_____123 TO 4622 OF HUMAN CFTR CDNA_____2580i_____2590>
 3070 3080 3090 3100 3110 3120
 TAAGTGAAGA AATTAACGAA GAAGACTTAA AGGAGTGCCT TTTTGATGAT ATGGAGAGCA
 ATTCACCTCT TTAATTGCTT CTTCTGAATT TCCTCAGCGA AAACTACTA TACCTCTCGT
 I S E E I N E E D L K E C L F D D M E S>
 _____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON_____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
 _____2600i_____123 TO 4622 OF HUMAN CFTR CDNA_____2640i_____2650>
 3130 3140 3150 3160 3170 3180
 TACCAGCAGT GACTACATGG AACACATACC TTCGATATAT TACTGTCCAC AAGAGCTTAA
 ATGGTCGTCA CTGATGTACC TTGTGTATGG AAGCTATATA ATGACAGGTG TTCTCGAATT
 I P A V T T W N T Y L R Y I T V H K S L>
 _____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON_____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
 _____2660i_____123 TO 4622 OF HUMAN CFTR CDNA_____2700i_____2710>
 3190 3200 3210 3220 3230 3240
 TTTTGTGCT AATTTGGTGC TTAGTAATTT TTCTGGCAGA GGTGGCTGCT TCCTTGGTGTG
 AAAAACACGA TTAACCACG AATCATTAAA AAGACCGTCT CCACCGACGA AGAAACCAAC
 I F V L I W C L V I F L A E V A A S L V>
 _____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON_____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
 _____2720i_____123 TO 4622 OF HUMAN CFTR CDNA_____2760i_____2770>
 3250 3260 3270 3280 3290 3300
 TGCTGTGGCT CCTTGGAAC ACTCCTCTTC AAGACAAAGG GAATAGTACT CATAGTAGAA
 ACGACACCGA GGAACCTTTG TGAGGAGAAG TTCTGTTTCC CTATCATGA GTATCATCTT
 V L W L L G N T P L Q D K G N S T H S R>
 _____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON_____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
 _____2780i_____123 TO 4622 OF HUMAN CFTR CDNA_____2820i_____2830>
 3310 3320 3330 3340 3350 3360
 ATAACAGCTA TGCAGTGATT ATCACCAGCA CCAGTTCGTA TTATGTGTTT TACATTTACG
 TATTGTCGAT ACGTCACTAA TAGTGTCGT GGTCAAGCAT AATACACAAA ATGTAAATGC
 N N S Y A V I I T S T S S Y Y V F Y I Y>
 _____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON_____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
 _____2840i_____123 TO 4622 OF HUMAN CFTR CDNA_____2880i_____2890>
 3370 3380 3390 3400 3410 3420
 TGGGAGTAGC CGACACTTTG CTTGCTATGG GATTCTTCAG AGGTCTACCA CTGGTGCATA
 AACTTCATCG GCTGTGAAAC GAACGATACC CTAAGAAGTC TCCAGATGGT GACCACGTAT
 V G V A D T L L A M G F F R G L P L V H>
 _____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON_____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
 _____2900i_____123 TO 4622 OF HUMAN CFTR CDNA_____2940i_____2950>
 3430 3440 3450 3460 3470 3480
 CTCTAATCAC AGTGTGCAAA ATTTTACACC ACAAATGTT ACATTCTGTT CTTCAAGCAC
 GAGATTAGTG TCACAGCTTT TAAAATGTGG TGTTTTACAA TGTAAGACAA GAAGTTCGTG
 T L I T V S K I L H H K M L H S V L Q A>
 _____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON_____>

_____h_____HYBRID ELA-CFTR-ElB MESSAGE _____h_____>
 _____2960i_____123 TO 4622 OF HUMAN CFTR CDNA _____3000i_____3010>

3490 3500 3510 3520 3530 3540

CTATGTCAAC CCTCAACACG TTGAAAGCAG GTGGGATTCT TAATAGATTTC TCCAAAGATA
 GATACAGTTG GGAGTTGTGC AACTTTCGTC CACCCTAAGA ATTATCTAAG AGGTTTCTAT
 P M S T L N T L K A G G I L N R F S K D>

____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>

_____h_____HYBRID ELA-CFTR-ElB MESSAGE _____h_____>
 _____3020i_____123 TO 4622 OF HUMAN CFTR CDNA _____3060i_____3070>

3550 3560 3570 3580 3590 3600

TAGCAATTTT GGATGACCTT CTGCCTCTTA CCATATTTGA CTTCATCCAG TTGTTATTAA
 ATCGTTAAAA CCTACTGGAA GACGGAGAAT GGTATAAACT GAAGTAGGTC AACAATAATT
 I A I L D D L L P L T I F D F I Q L L L>

____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>

_____h_____HYBRID ELA-CFTR-ElB MESSAGE _____h_____>
 _____3080i_____123 TO 4622 OF HUMAN CFTR CDNA _____3120i_____3130>

3610 3620 3630 3640 3650 3660

TTGTGATTGG AGCTATAGCA GTTGTCCGAG TTTTACAACC CTACATCTTT GTTGCAACAG
 AACACTAACC TCGATATCGT CAACAGCGTC AAAATGTTGG GATGTAGAAA CAACGTTGTC
 I V I G A I A V V A V L Q P Y I F V A T>

____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>

_____h_____HYBRID ELA-CFTR-ElB MESSAGE _____h_____>
 _____3140i_____123 TO 4622 OF HUMAN CFTR CDNA _____3180i_____3190>

3670 3680 3690 3700 3710 3720

TGCCAGTGAT AGTGGCTTTT ATTATGTTGA GAGCATATTT CCTCCAAACC TCACAGCAAC
 ACGGTCAC TAACCGAAAA TAATACAAC CTCGTATAAA GGAGGTTTGG AGTGTCTGTTG
 V P V I V A F I M L R A Y F L Q T S Q Q>

____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>

_____h_____HYBRID ELA-CFTR-ElB MESSAGE _____h_____>
 _____3200i_____123 TO 4622 OF HUMAN CFTR CDNA _____3240i_____3250>

3730 3740 3750 3760 3770 3780

TCAAACAACCT GGAATCTGAA GGCAGGAGTC CAATTTTCAC TCATCTTGTT ACAAGCTTAA
 AGTTTGTGTA CCTTAGACTT CCGTCCTCAG GTTAAAAGTG AGTAGAACAA TGTTCCGATT
 L K Q L E S E G R S P I F T H L V T S L>

____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>

_____h_____HYBRID ELA-CFTR-ElB MESSAGE _____h_____>
 _____3260i_____123 TO 4622 OF HUMAN CFTR CDNA _____3300i_____3310>

3790 3800 3810 3820 3830 3840

AAGGACTATG GACACTTCGT GCCTTCGGAC GGCAGCCTTA CTTTGAAACT CTGTTCCACA
 TTCCTGATAC CTGTGAAGCA CGGAAGCCTG CCGTCGGAAT GAAACTTTGA GACAAGGTGT
 K G L W T L R A F G R Q P Y F E T L F H>

____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>

_____h_____HYBRID ELA-CFTR-ElB MESSAGE _____h_____>
 _____3320i_____123 TO 4622 OF HUMAN CFTR CDNA _____3360i_____3370>

3850 3860 3870 3880 3890 3900

AAGCTCTGAA TTTACATACT GCCAACTGGT TCTTGACCT CTCACACTG CGCTGCTTCC
 TTCGAGACTT AAATGTATGA CGTTTGACCA AGAACATGGA CAGTTGTGAC GCGACCAAGG
 K A L N L H T A N W F L Y L S T L R W F>

____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
 _____3380i_____123 TO 4622 OF HUMAN CFTR CDNA_____3420i_____3430>

3910 3920 3930 3940 3950 3960
 AAATGAGAAT AGAAATGATT TTTGTCATCT TCTTCATTGC TGTACCTTC ATTTCCATTT
 TTTACTCTTA TCTTTACTAA AAACAGTAGA AGAAGTAACG ACAATGGAAG TAAAGGTAAA
 Q M R I E M I F V I F F I A V T F I S I>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
 _____3440i_____123 TO 4622 OF HUMAN CFTR CDNA_____3480i_____3490>

3970 3980 3990 4000 4010 4020
 TAACAACAGG AGAAGGAGAA GGAAGAGTTG GTATTATCCT GACTTTAGCC ATGAATATCA
 ATTGTTGTCC TCTTCTCTT CCTTCTCAAC CATAATAGGA CTGAAATCGG TACTTATAGT
 L T T G E G E G R V G I I L T L A M N I>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
 _____3500i_____123 TO 4622 OF HUMAN CFTR CDNA_____3540i_____3550>

4030 4040 4050 4060 4070 4080
 TGAGTACATT GCAGTGGGCT GTAAACTCCA GCATAGATGT GGATAGCTTG ATGCGATCTG
 ACTCATGTAA CGTCACCCGA CATTGAGGT CGTATCTACA CCTATCGAAC TACGCTAGAC
 M S T L Q W A V N S S I D V D S L M R S>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
 _____3560i_____123 TO 4622 OF HUMAN CFTR CDNA_____3600i_____3610>

4090 4100 4110 4120 4130 4140
 TGAGCCGAGT CTTTAAGTTC ATTGACATGC CAACAGAAGG TAAACCTACC AAGTCAACCA
 ACTCGGCTCA GAAATTCAAG TAACTGTACG GTTGTCTTCC ATTTGGATGG TTCAGTTGGT
 V S R V F K F I D M P T E G K P T K S T>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
 _____3620i_____123 TO 4622 OF HUMAN CFTR CDNA_____3660i_____3670>

4150 4160 4170 4180 4190 4200
 AACCATACAA GAATGGCCAA CTCTCGAAG TTATGATTAT TGAGAATTCA CACGTGAAGA
 TTGGTATGTT CTTACCGGTT GAGAGCTTTC AATACTAATA ACTCTTAAGT GTGCACTTCT
 K P Y K N G Q L S K V M I I E N S H V K>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
 _____3680i_____123 TO 4622 OF HUMAN CFTR CDNA_____3720i_____3730>

4210 4220 4230 4240 4250 4260
 AAGATGACAT CTGGCCCTCA GGGGGCCAAA TGA CTGTCAA AGATCTCACA GCAAAATACA
 TTCTACTGTA GACCGGGAGT CCCCCGGTTT ACTGACAGTT TCTAGAGTGT CGTTTTATGT
 K D D I W P S G G Q M T V K D L T A K Y>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h_____>
 _____3740i_____123 TO 4622 OF HUMAN CFTR CDNA_____3780i_____3790>

4270 4280 4290 4300 4310 4320
 CAGAAGGTGS AAATGCCATA TTAGAGAAC TTTCTTTCTC AATAAGTCCT GGCCAGAGGC
 GTCTTCCACC TTTACGGTAT AATCTCTTGT AAAGGAGAG TTATTTCAGGA CCGGTCTCCC

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T E G G N A I L E N I S F S I S P G Q R>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID E1A-CFTR-E1B MESSAGE____h____>
 ____3800i____123 TO 4622 OF HUMAN CFTR CDNA____3840i____3850>
 4330 4340 4350 4360 4370 4380
 TGGGCCTCTT GGAAGAACT GGATCAGGA AGAGTACTTT GTTATCAGCT TTTTGTAGAC
 ACCCGGAGAA CCCTTCTTGA CCTAGTCCCT TCTCATGAAA CAATAGTCGA AAAAAGTCTG
 V G L L G R T G S G K S T L L S A F L R>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID E1A-CFTR-E1B MESSAGE____h____>
 ____3860i____123 TO 4622 OF HUMAN CFTR CDNA____3900i____3910>
 4390 4400 4410 4420 4430 4440
 TACTGAACAC TGAAGGAGAA ATCCAGATCG ATGGTGTGTC TTGGGATTCA ATAAGTTTGC
 ATGACTTGTG ACTTCCTCTT TAGGTCTAGC TACCACACAG AACCCCTAAGT TATTGAAACG
 L L N T E G E I Q I D G V S W D S I T L>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID E1A-CFTR-E1B MESSAGE____h____>
 ____3920i____123 TO 4622 OF HUMAN CFTR CDNA____3960i____3970>
 4450 4460 4470 4480 4490 4500
 AACAGTGGAG GAAAGCCTTT GGAGTGATAC CACAGAAAGT ATTTATTTTT TCTGGAACAT
 TTGTCACCTG CTTTCGGAAA CCTCACTATG GTGTCTTTCA TAAATAAAAA AGACCTTGTA
 Q Q W R K A F G V I P Q K V F I F S G T>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID E1A-CFTR-E1B MESSAGE____h____>
 ____3980i____123 TO 4622 OF HUMAN CFTR CDNA____4020i____4030>
 4510 4520 4530 4540 4550 4560
 TTAGAAAAAA CTTGGATCCC TATGAACACT GGAGTGATCA AGAAATATGG AAAGTTGCAG
 AATCTTTTTT GAACCTAGGG ATACTTGTC AACTCACTAGT TCTTTATACC TTTCAACGTC
 F R K N L D P Y E Q W S D Q E I W K V A>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID E1A-CFTR-E1B MESSAGE____h____>
 ____4040i____123 TO 4622 OF HUMAN CFTR CDNA____4080i____4090>
 4570 4580 4590 4600 4610 4620
 ATGAGSTTGS GCTCAGATCT GTGATAGAAC AGTTTCCTGG GAAGCTTGAC TTTGTCTTGG
 TACTCCAACC CGAGTCTAGA CACTATCTTG TCAAGGACC CTTTGAAGCTG AAACAGGPAAC
 D E V G L R S V I E Q F P G K L D F V L>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID E1A-CFTR-E1B MESSAGE____h____>
 ____4100i____123 TO 4622 OF HUMAN CFTR CDNA____4140i____4150>
 4630 4640 4650 4660 4670 4680
 TGGATGGGGG CTGTGTCCTA AGCCATGGCC ACAGCAGTT GATGTGCTTG GCTAGATCTG
 ACCTACCCCC GACACAGGAT TCGGTACCCG TCTTCGTCAA CTACACGAAC CGATCTAGAC
 V D G G C V L S H G H K Q L M C L A R S>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID E1A-CFTR-E1B MESSAGE____h____>
 ____4160i____123 TO 4622 OF HUMAN CFTR CDNA____4200i____4210>
 4690 4700 4710 4720 4730 4740
 TTCTCAGTAA GCGGAAGATC TTGCTGCTTG ATTAATTCAG TGGTCAATTTG GATCCAGTAA

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AAGAGTCATT CCGCTTCTAG AACGACGAAC TACTTGGGTC ACGAGTAAAC CTAGGTCATT
 V L S K A K I L L L D E P S A H L D P V>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ElB MESSAGE ____h____>
 ____4220i____123 TO 4622 OF HUMAN CFTR CDNA ____4260i____4270>

4750 4760 4770 4780 4790 4800

CATACCAAT AATTAGAAGA ACTCTAAAAC AAGCATTTCG TGATTGCACA GTAATTCTCT
 GTATGGTTTA TTAATCTTCT TGAGATTTTG TTCGTAAACG ACTAACGTGT CATTAAGAGA
 T Y Q I I R R T L K Q A F A D C T V I L>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ElB MESSAGE ____h____>
 ____4280i____123 TO 4622 OF HUMAN CFTR CDNA ____4320i____4330>

4810 4820 4830 4840 4850 4860

GTGAACACAG GATAGAAGCA ATGCTGGAAT GCCAACAATT TTTGGTCATA GAAGAGAACA
 CACTTGTGTC CTATCTTCGT TACGACCTTA CGTTTGTTAA AAACCAGTAT CTTCTCTTGT
 C E H R I E A M L E C Q Q F L V I E E N>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ElB MESSAGE ____h____>
 ____4340i____123 TO 4622 OF HUMAN CFTR CDNA ____4380i____4390>

4870 4880 4890 4900 4910 4920

AAGTGCGGCA GTACGATTCC ATCCAGAAAC TGCTGAACGA GAGGAGCCTC TTCCGGCAAG
 TTCACGCCGT CATGCTAAGG TAGGTCTTTG ACGACTTGCT CTCCTCGGAG AAGGCCGTTC
 K V R Q Y D S I Q K L L N E R S L F R Q>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ElB MESSAGE ____h____>
 ____4400i____123 TO 4622 OF HUMAN CFTR CDNA ____4440i____4450>

4930 4940 4950 4960 4970 4980

CCATCAGCCC CTCCGACAGG GTGAAGCTCT TTCCCCACCG GAACTCAAGC AAGTGCAAGT
 GGTAGTCGGG GAGGCTGTCC CACTTCGAGA AAGGGGTGGC CTTGAGTTTCG TTCACGTTCA
 A I S P S D R V K L F P H R N S S K C K>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ElB MESSAGE ____h____>
 ____4460i____123 TO 4622 OF HUMAN CFTR CDNA ____4500i____4510>

4990 5000 5010 5020 5030 5040

CTAAGCCCCA GATTGCTGCT CTGAAGAGG AGACAGAAGA AGAGGTGCAA GATACAAGGC
 GATTGGGSGT CTAACGACGA GACTTCTTCC TCTGTCTTCT TCTCCACGTT CTATGTTCCG
 S K P Q I A A L K E E T E E E V Q D T R>
 ____CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; CODON____>
 ____h____HYBRID ELA-CFTR-ElB MESSAGE ____h____>
 ____4520i____123 TO 4622 OF HUMAN CFTR CDNA ____4560i____4570>

5050 5060 5070 5080 5090 5100

TTTAGAGAGC AGCATAAATG TTGACATGGG ACATTTGCTC ATGGAATTGG AGGTAGCGGA
 AAATCTCTCG TCGTATTTAC AACTGTACCC TGTAACGAG TACCTTAACC TCCATCGCCT
 L >

____h____HYBRID ELA-CFTR-ElB MESSAGE ____h____>

____4580i____123 TO 4622 OF HUMAN CFTR CDNA ____4620i____>

5110 5120 5130 5140 5150 5160
 TTGAGGTACT GAAATGTGTG GCGGTGGCTT AAGGGTGGGA AAGAATATAT AAGGTGGGGG
 AACTCCATGA CTTTACACAC CCGCACCGAA TTCCACCCTT TCCTTATATA TTCCACCCCC
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h____>
 _____10_g_____ELB 3' UNTRANSLATED SEQUENCES _____50_g_____60____>
 _____k_____10_____k_____ELB 3' INTRON _____k_____40_____k_____50____>

5170 5180 5190 5200 5210 5220
 TCTCATGTAG TTTTGTATCT GTTTTGCAGC AGCCGCCGCC ATGAGCGCCA ACTCGTTTGA
 AGAGTACATC AAAACATAGA CAAAACGTCG TCGGCGGCGG TACTCGCGGT TGAGCAAAC
 _____M_____S_____A_____N_____S_____F_____D____>
 _____IX PROTEIN (HE_____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h____>
 _____l_____l_____IX MRNA _____l_____l_____>
 _____70_g_____ELB 3' UNTRANSLATED SEQUENCES _____110_g_____120____>
 _____60_g_____ELB 3' INTRON _____80____>

5230 5240 5250 5260 5270 5280
 TGGAAGCATT GTGAGCTCAT ATTTGACAAC GCGCATGCCC CCATGGGCCG GGGTGCCTCA
 ACCTTCGTAA CACTCGAGTA TAAACTGTTG CGCGTACGGG GGTACCCGGC CCCACGCAGT
 G S I V S S Y L T T R M P P W A G V R Q>
 _____IX PROTEIN (HEXON-ASSOCIATED PROTEIN); CODON_START=1____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h____>
 _____l_____l_____IX MRNA _____l_____l_____>
 _____130_g_____ELB 3' UNTRANSLATED SEQUENCES _____170_g_____180____>

5290 5300 5310 5320 5330 5340
 GAATGTGATG GGCTCCAGCA TTGATGGTCG CCGGCTCCTG CCGCAAACCT CTACTACCTT
 CTTTACACTAC CCGAGGTCGT AACTACCAGC GGGGCAGGAC GGGCGTTTGA GATGATGGAA
 N V M G S S I D G R P V L P A N S T T L>
 _____IX PROTEIN (HEXON-ASSOCIATED PROTEIN); CODON_START=1____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h____>
 _____l_____l_____IX MRNA _____l_____l_____>
 _____190_g_____ELB 3' UNTRANSLATED SEQUENCES _____230_g_____240____>

5350 5360 5370 5380 5390 5400
 GACCTACGAG ACCGTGTCTG GAACGCCGTT GGAGACTGCA GCCTCCGCCG CCGCTTCAGC
 CTGGATGCTC TGGCAGAGAC CTTGCGGCAA CTTCTGACGT CGGAGGCGGC GGCGAAGTCG
 T Y E T V S G T P L E T A A S A A A S A>
 _____IX PROTEIN (HEXON-ASSOCIATED PROTEIN); CODON_START=1____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h____>
 _____l_____l_____IX MRNA _____l_____l_____>
 _____250_g_____ELB 3' UNTRANSLATED SEQUENCES _____290_g_____300____>

5410 5420 5430 5440 5450 5460
 CGCTGCAGCC ACCGCCCGCG GGATTGTGAC TGACTTTGCT TTCCTGAGCC CGCTTGCAAG
 GCGACGTCGG TGGCGGCGCG CTTAACAATG ACTGAAACGA AAGGACTCGG GCGAAGCTTC
 A A A T A R G I V T D F A F L S P L A S>
 _____IX PROTEIN (HEXON-ASSOCIATED PROTEIN); CODON_START=1____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE _____h____>
 _____l_____l_____IX MRNA _____l_____l_____>
 _____310_g_____ELB 3' UNTRANSLATED SEQUENCES _____350_g_____360____>

5470 5480 5490 5500 5510 5520
 CAGTGCAGCT TCCCGTTTAT CCGCCCGCGA TGACAAGTTG ACGGCTCTTT TGGCACAATT

GTCACGTCGA AGGGCAAGTA GCGGGGCGCT ACTGTTCAAC TGCCGAGAAA ACCGTGTTAA
 S A A S R S S A R D D K L T A L L A Q L>
 _____IX PROTEIN (HEXON-ASSOCIATED PROTEIN); CODON_START=1____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE_____h____>
 _____l_____l_____IX MRNA_____l_____l____>
 _____370_g_____ELB 3' UNTRANSLATED SEQUENCES_____410_g_____420____>

5530 5540 5550 5560 5570 5580
 GGATTCTTTG ACCCGGGAAC TTAATGTCGT TTCTCAGCAG CTGTTGGATC TGCGCCAGCA
 CCTAAGAAAC TGGGCCCTTG AATTACAGCA AAGAGTCGTC GACAACCTAG ACGCGGTCGT
 D S L T R E L N V V S Q Q L L D L R Q Q>
 _____IX PROTEIN (HEXON-ASSOCIATED PROTEIN); CODON_START=1____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE_____h____>
 _____l_____l_____IX MRNA_____l_____l____>
 _____430_g_____ELB 3' UNTRANSLATED SEQUENCES_____470_g_____480____>

5590 5600 5610 5620 5630
 GGTTCCTGCC CTGAAGGCTT CCTCCCCTCC CAATGCGGTT TAAACATAA ATAAA
 CCAAAGACGG GACTCCGAA GGAGGGGAGG GTTACGCCAA ATTTGTATT TATTT
 V S A L K A S S P P N A V *>
 _____IX PROTEIN (HEXON-ASSOCIATED PROTEIN); C____>
 _____h_____HYBRID ELA-CFTR-ELB MESSAGE_____h____>
 _____l_____l_____IX MRNA_____l_____l____>
 _____490_g_____ELB 3' UNTRANSLATED SEQUENCES_____530_g_____>

Table III

Nucleotide Sequence Analysis of Ad2-ORF6/PGK-CFTR

LOCUS	AD2-ORF6/P 36335 BP DS-DNA		
DEFINITION	-		
ACCESSION	-		
KEYWORDS	-		
SOURCE	-		
FEATURES	From	To/Span	Description
frag	12915	36335	10676 to 34096 of Ad2-E4/ORF6
frag	35069	35973	33178 to 34082 of Ad2 seq
pre-msg >	35973	< 35069 (C)	E4 mRNA [Nucleic Acids Res. 9, 1675-1689 (1981)], [J. Mol. Biol. 149, 189-221 (1981)], [Nucleic Acids Res. 12, 3503-3519 (1984)], [Unpublished (1984)] [Split]
IVS	35794	35084 (C)	E4 mRNA intron D7 [J. Virol. 50, 106-117 (1984)], [Nucleic Acids Res. 12, 3503-3519 (1984)], [Unpublished (1984)]
IVS	35794	35175 (C)	E4 mRNA intron D6 [Nucleic Acids Res. 12, 3503-3519 (1984)]
IVS	35794	35268 (C)	E4 mRNA intron D5 [J. Virol. 50, 106-117 (1984)]
IVS	35794	35295 (C)	E4 mRNA intron D4 [J. Virol. 50, 106-117 (1984)]
IVS	35794	35343 (C)	E4 mRNA intron D3 [J. Virol. 50, 106-117 (1984)]
IVS	35794	35501 (C)	E4 mRNA intron D2 [J. Virol. 50, 106-117 (1984)]
IVS	35794	35570 (C)	E4 mRNA intron D1 [J. Virol. 50, 106-117 (1984)]
IVS	35794	35766 (C)	E4 mRNA intron D [J. Virol. 50, 106-117 (1984)]
frag	35978	36335	35580 to 35937 of Ad2 seq
pre-msg	36007	< 35978 (C)	E4 mRNA [Nucleic Acids Res. 9, 1675-1689 (1981)], [J. Mol. Biol. 149, 189-221 (1981)], [Nucleic Acids Res. 12, 3503-3519 (1984)], [Unpublished (1984)] [Split]
rpt	36234	36335	inverted terminal repetition; 99.54% [Biochem. Biophys. Res. Commun. 87, 671-678 (1979)], [J. Mol. Biol. 128, 577-594 (1979)]
frag	~ 12915	35054	1 to 32815 of Ad2 seq [Split]
pept	< 28478	28790	3 33K protein (virion morphogenesis)
pept	28478	28790	1 33K protein (virion morphogenesis); codon_start=1
mRNA	29331	< 12915 (C)	E2b mRNA [J. Biol. Chem. 257, 13475-13491 (1982)] [Split]
pre-msg <	12915	16352	major late mRNA L1 (alt.) [J. Mol. Biol. 149, 189-221 (1981)], [J. Virol. 48, 127-134 (1983)] [Split]
pre-msg <	12915	20208	major late mRNA L2 (alt.) [J. Mol. Biol. 149, 189-221 (1981)], [J. Virol. 38, 469-482 (1981)], [J. Virol. 48, 127-134 (1983)] [Split]
pre-msg <	12915	24682	major late mRNA L3 (alt.) [Nucleic Acids Res. 9, 1-17 (1981)], [J. Mol. Biol. 149, 189-221 (1981)], [J. Virol. 48, 127-134 (1983)] [Split]
pre-msg <	12915	30462	major late mRNA L4 (alt.) [J. Mol. Biol. 149, 189-221 (1981)], [J. Virol. 48, 127-134 (1983)] [Split]
pre-msg <	12915	35037	major late mRNA L5 (alt.) [J. Mol. Biol. 149, 189-221 (1981)], [J. Virol. 48, 127-134 (1983)] [Split]

Nucleotide Sequence Analysis (cont.)

mRNA	< 12915	13278	major late mRNA intron (precedes 52,55K mRNA; 1st L1 mRNA) [Cell 16, 841-850 (1979)], [Cell 16, 851-861 (1979)], [J. Mol. Biol. 134, 143-158 (1979)], [J. Mol. Biol. 135, 413-433 (1979)], [Nature 292, 420-426 (1981)] [Split]
IVS	< 12915	16388	major late mRNA intron (precedes penton mRNA; 1st L2 mRNA) [J. Virol. 48, 127-134 (1983)] [Split]
IVS	< 12915	18754	major late mRNA intron (precedes pV mRNA; 2nd L2 mRNA) [J. Biol. Chem. 259, 13980-13985 (1984)] [Split]
IVS	< 12915	20238	major late mRNA intron (precedes pVI mRNA; 1st L3 mRNA) [J. Virol. 38, 469-482 (1981)] [Split]
IVS	< 12915	21040	major late mRNA intron (precedes hexon mRNA; 2nd L3 mRNA) [Proc. Natl. Acad. Sci. U.S.A. 75, 5822-5826 (1978)], [Cell 16, 841-850 (1979)] [Split]
IVS	< 12915	23888	major late mRNA intron (precedes 23K mRNA; 3rd L3 mRNA) [Nucleic Acids Res. 9, 1-17 (1981)] [Split]
IVS	< 12915	26333	major late mRNA intron (precedes 100K mRNA; 1st L4 mRNA) [Virology 128, 140-153 (1983)] [Split]
RNA	< 12915	13005	VA I RNA (alt.) [J. Biol. Chem. 252, 9043-9046 (1977)] [Split]
RNA	< 12915	13005	VA I RNA (alt.) [J. Biol. Chem. 246, 6991-7009 (1971)], [J. Biol. Chem. 252, 9047-9054 (1977)], [Proc. Natl. Acad. Sci. U.S.A. 77, 2424-2428 (1980)] [Split]
????	< 12915	13262	VA II RNA [Proc. Natl. Acad. Sci. U.S.A. 77, 3778-3782 (1980)], [Proc. Natl. Acad. Sci. U.S.A. 77, 2424-2428 (1980)] [Split]
pept	13279	14526	1 52,55K protein; codon_start=1
pept	14547	16304	1 IIIa protein (peripentonal hexon-associated protein; splice sites not sequenced); codon_start=1
signal	16331	16336	major late mRNA L1 poly-A signal (putative) 39.21%
pept	16390	18105	1 penton protein (virion component III); codon_start=1
pept	18112	18708	1 Pro-VII protein (precursor to major core protein); codon_start=1
pept	18778	19887	1 pV protein (minor core protein); codon_start=1
signal	20188	20193	major late mRNA L2 polyadenylation signal (putative) 49.94%
pept	20240	20992	1 pVI protein (hexon-associated precursor); codon_start=1
pept	21077	23983	1 hexon protein (virion component II); codon_start=1
????	< 12915	24631	23K protein (endopeptidase); codon_start=1 [Split]
signal	24657	24662	major late mRNA L3 polyadenylation signal (putative); 62.38%
pre-msg	28193	24659 (C)	E2a late mRNA (alt.) [J. Mol. Biol. 149, 189-221 (1981)]
pre-msg	28195	24659 (C)	E2a late mRNA (alt.) [Nucleic Acids Res. 12, 3503-3519 (1984)], [Unpublished (1984)]
pre-msg	29330	24659 (C)	E2a early mRNA (alt.) [J. Mol. Biol. 149,

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Nucleotide Sequence Analysis (cont.)

			189-221 (1981)]
pre-msg	29331	24659 (C)	E2a early mRNA (alt.) [J. Mol. Biol. 149, 189-221 (1981)]
signal	24683	24678 (C)	E2a mRNA polyadenylation signal on comp strand (putative); 62.43%
pept	26318	24729 (C1	DBP protein (DNA binding or 72K protein); codon_start=1
IVS	26953	26328 (C)	E2a mRNA intron B [Nucleic Acids Res. 9, 4439-4457 (1981)]
pept	26347	28764 1	100K protein (hexon assembly); codon_start=1
IVS	29263	27031 (C)	E2a early mRNA intron A [Cell 18, 569-580 (1979)]
IVS	28124	27211 (C)	E2a late mRNA intron A [Virology 128, 140-153 (1983)]
IVS	28791	28992	33K-pept intron [J. Virol. 45, 251-263 (1983)]
pept	28993	> 29366 1	33K protein (virion morphogenesis)
pept	29454	30137 1	pVIII protein (hexon-associated precursor); codon_start=1
mRNA	29848	33103	E3-2 mRNA; 85.88% [Gene 22, 157-165 (1983)]
IVS	30220	30614	major late mRNA intron ('x' leader) [Gene 22, 157-165 (1983)], [J. Biol. Chem. 259, 13980-13985 (1984)]
signal	30444	30449	major late mRNA L4 polyadenylation signal; (putative) 78.48%
signal	< 12915	32676	major late mRNA intron ('y' leader) [J. Mol. Biol. 135, 413-433 (1979)], [J. Virol. 38, 469-482 (1981)], [EMBO J. 1, 249-254 (1982)], [Gene 22, 157-165 (1983)] [Split]
pept	31051	31530 1	E3 19K protein (glycosylated membrane protein); codon_start=1
pept	31707	32012 1	E3 11.6K protein; codon_start=1
signal	32008	32013	E3-1 mRNA polyadenylation signal (putative); 82.69%
IVS	32822	33268	major late mRNA intron ('z' leader) [Proc. Natl. Acad. Sci. U.S.A. 75, 5822-5826 (1978)], [Cell 16, 841-850 (1979)], [EMBO J. 1, 249-254 (1982)], [Gene 22, 157-165 (1983)]
signal	33081	33086	E3-2 mRNA polyadenylation signal; 85.82% (putative)
????	< 12915	35017	fiber protein (virion component IV); codon_start=1 [Split]
signal	35013	35018	major late mRNA L5 polyadenylation signal; (putative) 91.19%
pre-msg	35054	> 35041 (C)	E4 mRNA [Nucleic Acids Res. 9, 1675-1689 (1981)], [J. Mol. Biol. 149, 189-221 (1981)], [Nucleic Acids Res. 12, 3503-3519 (1984)], [Unpublished (1984)] [Split]
frag	1	12914	1 to 12914 of pAd2/PGK-CFTR
DNA	1	> 356	1 to 357 Ad2
rpt	1	> 103	inverted terminal repetition; 0.28% [Biochem. Biophys. Res. Commun. 87, 671-678 (1979)], [J. Mol. Biol. 128, 577-594 (1979)]
	< 10	103	inverted terminal repetition; 0.28% [Biochem. Biophys. Res. Commun. 87, 671-678 (1979)], [J. Mol. Biol. 128, 577-594 (1979)] [Split]
frag	357	379	linker segment
frag	915	> 923	polylinker cloning sites [Split]

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Nucleotide Sequence Analysis (cont.)

	<	924	>	954	polylinker cloning sites [Split]
DNA	<	5567	>	12914	3328 to 10685 of Ad2 [Split]
signal		380		914	pgk promoter
frag	<	955	>	958	polylinker cloning sites [Split]
	<	5501		5522	polylinker cloning sites [Split]
signal		5523		5555	syn. BGH poly A
frag		5555	>	5560	linker [Split]
	<	5564		5567	linker [Split]
frag		959		5500	920 to 5461 of pCMV-CFTR-936C
revision		2868		2868	mistake in published sequence of Riordan et al. C not A is correct = N to H a.a. change
modified		1814		1814	936 T to C mutation to inactivate cryptic bacterial promoter. Silent amino acid change
site	<	959		975	polylinker segment from pCMV-CFTR-936C
site		976		990	(Rc/CMV-Invitrogen SpeI-BstXI) [Split]
site		991		1001	linker segment from pCMV-CFTR-936C. Originally Sali/BstXI adaptor oligo 1499DS
					linker segment from pCMV-CFTR-936C. Originally from pMT-CFTR construction oligo 1247 RG -Sal I to Aval sites.
mRNA		1001	>	5500	123 to 4622 of HUMCFTR
pept		1011	>	5453	1 cystic fibrosis transmembrane conductance regulator; codon_start=1
BASE COUNT		8597 A	10000 C	9786 G	7952 T 0 OTHER
ORIGIN		?			

Ad2-ORF6/P Length: 36335 Sep 16, 1993 - 08:13 PM Check: 1664 ..

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1 CATCATCAAT AATATACCTT ATTTTGGATT GAAGCCAATA TGATAATGAG GGGGTGGAGT
61 TTGTGACGTG GCGCGGGGCG TGGGAACGGG GCGGGTGACG TAGTAGTGTG GCGGAAGTGT
121 GATGTTGCAA GTGTGGCGGA ACACATGTAA GCGCCGGATG TGGTAAAAGT GACGTTTTTG
181 GTGTGCGCGG GTGTATACGG GAAGTGACAA TTTTCGGCGG GTTTTAGGCG GATGTTGTAG
241 TAAATTGTTG CGTAACCAAG TAATGTTTGG CCATTTTCGC GGGAAACTG AATAAGAGGA
301 AGTGAAATCT GAATAATTCT GTGTTACTCA TAGCGCGTAA TATTTGTCTA GGGCGCTCG
361 AGGTGACGGG TCTATCGATA AGCTTGATAT CGAATTCGGG GCTTGGGTTT GCGCCTTTTC
421 CAAGGCAGCC CTGGGTTTGC GCAGGGACGC TCGCACATTC TTCACGTCCG TTCGCAGCGT CACCCGGATC
481 AGCGGCGCGG ACCCTGGGTC CCGTTGTGGG CCCCCCGGCG ACCTTCTCTC GTCCGCCCTT AAGTCGGGAA
541 TTCGCGCGTA CCCTTGTGGG GTGCCGGACG TGACAAACGG AAGCCGACAG TCTCACTAGT
601 GGTTCCTTGC GGTTCGCGGC GTGCCGGACG TGACAAACGG AAGCCGACAG TCTCACTAGT
661 ACCCTGCGAG ACCGACAGCG CCAGGAGACA ATGGCAGCGC GCCGACCGCG ATGGGCTGTG
721 GCCAATAGCG GCTGCTCAGC AGGCGCGCGC GAGAGCAGCG GCCGGGAAGG GCGCGTGGCG
781 GAGGCGGGGT GTGGGCGGGT AGTGTGGGCC CTGTTCTCTC CCGCGCGGTG TTCGCGATTC
841 TGCAAGCCTC CGGAGCGCAC GTGGGCGAGT GCGTCCCTCG TTGACCGAAT CACCGACCTC
901 TCTCCCCAGG ATCCACTAGT ATTAAATCGT ACCCCTAGTA TTTAAATCGT ACCCCTAGTA
961 ACGGCGCGCA GTGTGCTGCA GATATCAAAG TCGACGGTAC CCGAGAGACC ATGCAGAGGT
1021 CGCCTCTGGA AAAGGCCAGC GTTGTCTCCA AACTTTTTTT CAGCTGGACC AGACCAATTT
1081 TGAGGAAAGG ATACAGACAG CGCCTGGAAT TGTCAGACAT ATACCAAATC CCTTCTGTG
1141 ATTCTGCTGA CAATCTATC C?AAAATTGG AAGGAGAATG GGATAGAGAG CTGGCTTCAA
1201 AGAAAAATCC TAAACTCATT AATGCCCTTC GCGGATGTTT TTTCTGGAGA TTTATGTTCT
1261 ATGGAATCTT TTTATATTTA GGGGAAGTCA CCAAAGCAGT ACAGCCTCTC TTACTGGGAA
1321 GAATCATAGC TTCCTATGAC CCGGATAACA AGGAGGAACG CTCTATCGCG ATTTATCTAG
1381 GCATAGGCTT ATGCCTTCTC TTTATTGTGA GGACACTGCT CCTACACCCA GCCATTTTTG
1441 GCCTTCATCA CATTGGAATG CAGATGAGAA TAGCTATGTT TAGTTTGATT TATAAGAAGA
1501 CTMTAAAGCT GTCAAGCCGT GTTCTAGATA AAATAAGTAT TGGACAACCT GTTAGTCTCC
1561 TTTCCAACAA CCTGAACAAA TTTGATGAAG GACTTGCAAT GGCACATTTT GTGTGGATCG
1621 CTCCTTTGCA AGTGGCACTC CTCATGGGGC TAATCTGGGA GTTGTTACAG GCGTCTGCCT
1681 TCTGTGGACT TGGTTTCTTG ATAGTCTCTG CCCTTTTTTC GGCTGGGCTA GGGAGAATGA
1741 TGATGAAGTA CAGAGATCAG AGAGCTGGGA AGATCAGTGA AAGACTTGTG ATTACCTCAG
1801 AAATGATTGA AAACATCCAA TCTGTTAAGG CATACTGCTG GGAAGAAGCA ATGGAAAAAA

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Nucleotide Sequence Analysis (cont.)

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1861 TGATTGAAAA CTTAAGACAA ACAGAACTGA AACTGACTCG GAAGGCAGCC TATGTGAGAT
1921 ACTTCAATAG CTCAGCCTTC TTCCTCTCAG GGTTCCTTGT GGTGTTTTTA TCTGTGCTTC
1981 CCTATGCACT AATCAAAAGG ATCATCCTCC GGAAATATT CACCACCATC TCATTCTGCA
2041 TTGTTCTGCG CATGGCGGTC ACTCGGCAAT TTCCTGCGGC TGTACAAACA TGTATGACT
2101 CTCTTGGAGC AATAAACAAA ATACAGGATT TCTTACAAAA GCAAGAATAT AAGACATTGG
2161 AATATACTT AACGACTACA GAAGTAGTGA TGGAGAATGT AACAGCCTTC TGGGAGGAGG
2221 GATTTGGGGA ATTATTTGAG AAGCAAAAC AAAACAATAA CAATAGAAAA ACTTCTAATG
2281 GTGATGACAG CCTCTCTCTC AGTAATTTCT CACTTCTTGG TACTCCTGTC CTGAAAGATA
2341 TTAATTTCAA GATAGAAAGA GGACAGTTGT TGGCGGTTGC TGGATCCACT GGAGCAGGCA
2401 AGACTTCACT TCTAATGATG ATTATGGGAG AACTGGAGCC TTCAGAGGGT AAAATTAAGC
2461 ACAGTGAAG AATTTCAATC TGTTCTCAGT TTTCTGCGAT TATGCCTGGC ACCATTAAAG
2521 AAAATATCAT CTTTGGTGT TCTATGATG AATATAGATA CAGAAGCGTC ATCAAAGCAT
2581 GCCAATGAGA AGAGGACATC TCCAGTTTG CAGAGAAAGA CAATATAGTT CTTGAGAGAAG
2641 GTGGAATCAC ACTGAGTGGG GGTCAACGAG CAAGAATTTT TTTAGCAAGA GCAGTATACA
2701 AAGATGCTGA TTTGTATTTA TTAGACTCTC CTTTTGGATA CCTAGATGTT TTAACAGAAA
2761 AAGAAATATT TGAAAGCTGT GTCTGTAAAC TGATGGCTAA CAAAAC TAGG ATTTTGGTCA
2821 CTTCTAAAAT GGAACATTTA AAGAAAGCTG ACAAATATT AATTTTGCAT GAAGCTAGCA
2881 GCTATTTTTA TGGGACATTT TCAGAACTCC AAAATCTACA GCCAGACTTT AGCTCAAAAC
2941 TCATGGGATG TGATTCTTTC GACCAATTTA GTGCAGAAAG AAGAAATTCA ATCCTAACTG
3001 AGACCTTACA CCGTTTCTCA TTAGAAGGAG ATGCTCCTGT CTCCTGGACA GAAACAAAAA
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3121 CAATCAACTC TATACGAAAA TTTTCCATTG TGCAAAGAC TCCCTTACAA ATGAATGGCA
3181 TCGAAGAGGA TTCTGATGAG CCTTTAGAGA GAAGGCTGTC CTTAGTACCA GATTCGTAGC
3241 AGGGAGAGGC GATACTGCCT CGCATCAGCG TGATCAGCAC TGGCCCCACG CTTGAGGCAC
3301 GAAGGAGGCA GTCTGTCTG AACCTGATGA CACACTCAGT TAACCAAGGT CAGAACATTC
3361 ACOGAAAGAC AACAGCATCC ACACGAAAAG TGTCACTGGC CCCTCAGGCA AACTTGACTG
3421 AACTGGATAT ATATTCAAGA AGGTTATCTC AAGAACTGG CTTGGAAATA AGTGAAGAAA
3481 TTAACGAAGA AGACTTAAAG GAGTGCCCTT TTGATGATAT GGAGAGCATA CCAGCAGTGA
3541 CTACATGGAA CACATACCTT CGATATATTA CTGTCCACAA GAGCTTAATT TTTGTGCTAA
3601 TTTGGTGCTT AGTAATTTTT CTGGCAGAGG TGGCTGCTTC TTTGGTTGTG TTTGGGCTCC
3661 TTGGAAACAC TCCTCTTCAA GACAAAGGGA ATAGTACTCA TAGTAGAAAT AACAGCTATG
3721 CAGTGATTAT CACCAGCACC AGTTGCTATT ATGTGTTTTA CATTACGTG GGAGTAGCCG
3781 ACACTTTGCT TGCTATGGGA TTCTTCAGAG GTCTACCACT GGTGCATACT CTAATCACAG
3841 TGTCGAAAAT TTTACACCAC AAAATGTTAC ATTCTGTTCT TCAAGCACCT ATGTCAACCC
3901 TCAACACGTT GAAAGCAGGT GGGATTCTTA ATAGATTCTC CAAAGATATA GCAATTTTGG
3961 ATGACCTTCT GCCTCTTACC ATATTGACT TCATCCAGTT GTTATTAATT GATATTGGAG
4021 CTATAGCAGT TGTCGCAGTT TTACAACCTT ACATCTTTGT TGCAACAGTG CCAGTGATAG
4081 TGGCTTTTAT TATGTTGAGA GCATATTTCC TCCAACCTC ACAGCAACTC AAACAACCTG
4141 AATCTGAAGG CAGGAGTCCA ATTTTCACTC ATCTTGTTAC AAGCTTAAAA GGAATATGGA
4201 CACTTCGTGC CTTGGGACGG CAGCCTTACT TTGAAACTCT GTTCCACAAA GCTCTGAATT
4261 TACATACTGC CAACTGGTTC TTGTACCTGT CAACACTGCG CTGGTTCCAA ATGAGAATAG
4321 AAATGATTTT TGTCATCTTC TTCATTGCTG TTACCTTCAT TCCATTTTA ACAACAGGAG
4381 AAGGAGAAGG AAGAGTTGGT ATTATCCGTA CTTTAGCCAT GAATATCATG AGTACATTGC
4441 AGTGGGCTGT AAATCCAGC ATAGATGTGG ATAGCTTGAT GCGATCTGTG AGCCGAGTCT
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4681 ATGCCATATT AGAGAACATT TCCTTCTCAA TAAGTCTTGG CCAGAGGGTG GGCCTCTTGG
4741 GAAGAACTGG ATCAGGGAAG AGTACTTTGT TATCAGCTTT TTTGAGACTA CTGAACACTG
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5101 CGAAGATCTT GCTGCTTGAT GAACCCAGTG CTCATTGGGA TCCAGTAACA TACCAATAA
5161 TTAGAAGAAC TCTAAAACAA GCATTTGCTG ATTGCACAGT AATTCTCTGT GAACACAGGA
5221 TAGAAGCAAT GCTCGAATGC CAACAATTTT TGGTCATAGA AGAGAACAAA GTGCGGCAGT

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Nucleotide Sequence Analysis (cont.)

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5281 ACGATTCCAT CCAGAACTG CTGAACGAGA GGAGCCTCTT CCGGCAAGCC ATCAGCCCOCT
5341 CCGACAGGGT GAAGCTCTTT CCCCACCGGA ACTCAAGCAA GTGCAAGTCT AAGCCCCAGA
5401 TTGCTGCTCT GAAAGAGGAG ACAGAAGAAG AGGTGCAAGA TACAAGGCTT TAGAGAGCAG
5461 CATAAATGTT GACATGGGAC ATTTGCTCAT GGAATTGGAG AAATCGTACG CTTAGGACGC
5521 GTAATAAAAT GAGGAAATTG CATCGCATTG TCTGACCGGT TACGCGGGAA GGTGCTGAGG
5581 TACGATGAGA CCCGCACCAG GTGCAGACCC TGGAGTGTG GCGGTAAACA TATTAGGAAC
5641 CAGCCTGTGA TGCTGGATGT GACCGAGGAG CTGAGGCCCG ATCACTTGGT GCTGGCCTGC
5701 ACCCGCGCTG AGTTTGGCTC TAGCGATGAA GATACAGATT GAGGTACTGA AATGTGTGGG
5761 CGTGGCTTAA GGTGGGAAA GAATATATAA GGTGGGGGTC TCATGTAGTT TTGTATCTGT
5821 TTTGCAGCAG CCGCCGCCAT GAGOGCCAAC TCGTTTGATG GAAGCATTGT GAGCTCATAT
5881 TTGACAAOCG GCATGCCCCC ATGGGCGGG GTGCGTCAGA ATGTGATGGG CTCCAGCATT
5941 GGTCTCGCC CCGTCTGCC CGAAACTCT ACTACCTTGA CCTACGAGAC CGTGTCTGGA
6001 ACGCOGTTGG AGACTGCAGC CTCGCGCGCC GCTTCAGCCG CTGCAGCCAC CGCCGCGGG
6061 ATTGTGACTG ACTTTGCTTT CCTGAGCCCG CTTGCAAGCA GTGCAGCTTC CCGTTCATCC
6121 GCCCGCGATG ACAAGTTGAC GGCTCTTTTG GCACAATTGG ATTCTTTGAC CCGGGAACCT
6181 AATGTGCTTT CTCAGCAGCT GTTGGATCTG CGCCAGCAGG TTTCTGCCCT GAAGGCTTCC
6241 TCCCCTCCCA ATGCGGTTTA AAACATAAAT AAAAACCAGA CTCTGTTTGG ATTTTGATCA
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6361 GGTCTCGGTC GTTGAGGGTC CTGTGTATTT TTTCCAGGAC GTGGTAAAGG TGACTCTGGA
6421 TGTTCAAGTA CATGGGCATA AGCCCGTCTC TGGGGTGGAG GTAGCACCAC TGCAGAGCTT
6481 CATGCTGCGG GGTGGTGTG TAGATGATCC AGTCGTAGCA GGAGCGCTGG GCGTGGTGCC
6541 TAAAAATGTC TTTCAGTAGC AAGCTGATTG CCAGGGGCGG GCCCTTGGTG TAAGTGTTTA
6601 CAAAGCGGTT AAGCTGGGAT GGGTGATATC GTGGGGATAT GAGATGCATC TTGGACTGTA
6661 TTTTATAGTT GGCTATGTTT CCAGCCATAT CCTCGGGG ATTCTGTG TGAGATGCTA
6721 CCAGCAGG GTATCCGGTG CATTGGGAA ATTTGTCATG TAGCTTAGAA GGAATGCGT
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6841 TGGCAATGGG CCCACGGGCG GCGGCCTGGG OGAAGATATT TCTGGGATCA CTAACGTCAT
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7621 GGTCTGCTG GTGCTGAAGC GCTGCCGGTC TTGCGCCCTG GCGTCCGGCA GGTAGCATTT
7681 GACCATGGTG TCATAGTCCA GCCCCTCCGC GGCGTGGCCC TTGGCGGCGA GCTTGCCCTT
7741 GGAGGAGGCG CCGCAGGAGG GGCAGTGCAG ACTTTTAAGG GCGTAGAGCT TGGGCGCGAG
7801 AAATACCGAT TCCGGGGAGT AGGCATCCGC GCGCAGGCG CCTCAAAAACC AGGTTTCCCC CATGCTTTTT
7861 CACGAGCCAG GTGAGCTCTG GCOGTTGGG GTCAAAAACC AGGTTTCCCC CATGCTTTTT
7921 GATGCGTTTC TTACCTCTGG TTTCCATGAG CCGGTGTCCA CGCTCGGTGA CGAAAAGGCT
7981 GTCCGTGTCC CCGTATACAG ACTTGAGAGG CCTGTCTCTG AGGGTGTGTC CGCGGTCTC
8041 CTCGTATAGA AACTCGGACC ACTCTGAGAC GAAGGCTCGC GTCCAGGCCA GCACGAAGGA
8101 GGCTAAGTGG GAGGGGTAGC GGTCTGTTGTC CACTAGGGGG TCCACTCGCT CCAGGGTGTG
8161 AAGACACATG TCGCCCTCTT CCGCATCAAG GAAGGTGATT GGTTTATAGG TGTAGGCCAC
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8281 CTCTTCCGCA TCGCTGCTG CAGGGCCAG CTGTTGGGGT GAGTACTCCC TCTCAAAAGC
8341 GGGCATGACT TCTGCGCTAA GATTGTGAGT TTCCAAAAC GAGGAGGATT TGATATTCAC
8401 CTGGCCCGCG GTGATGCCTT TGAGGGTGGC CGCGTCCATC TGGTCAGAAA AGACAATCTT
8461 TTTGTTGTCA AGCTTGGTGG CAAACGACCC GTAGAGGGCG TTGGACAGCA ACTTGGCGAT
8521 GGAGCGCAGG GTTTGGTTTT TGTGCGGATC GGGCGGCTCC TTGGCCGCGA TTTGAGCTG
8581 CACGTATTGG CGCGCAACGC ACCGCCATTG GGGAAAGACG GTGGTGGGCT CGTGGGGCAC
8641 CAGGTGCACG CGCCAACGCG GGTGTGTCAG GGTGACAAGG TCAACGCTGG TGGCTACCTC

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Nucleotide Sequence Analysis (cont.)

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8821	CAGGCGCGCG	TCGAAGTAGT	CTATCTTGCA	TCCTTGCAAG	TCTAGCGCCT	GCTGCCATCC
8881	GCGGGCGGCA	AGCGGCGGCT	CGTATGGGTT	GAGTGGGGGA	CCCCATGGCA	TGCGGTGGGT
8941	GAGCGCGGAG	GCGTACATGC	CGCAAATGTC	GTAAACGTAG	AGGGGCTCTC	TGAGTATTCC
9001	AAGATATGTA	GGGTAGCATC	TTCCACCGCG	GATGCTGGCG	CGCACGTAAT	CGTATAGTTC
9061	GTGCGAGGGA	GCGAGGAGGT	CGGGACCGAG	GTTGCTACGG	GCGGGCTGCT	CTGCTCGGAA
9121	GACTATCTGC	CTGAAGATGG	CATGTGAGTT	GGATGATATG	GTTCGACGCT	GGAAGACGTT
9181	GAAGTCGGCG	TCTGTGAGAC	CTACCGCGTC	ACGCACGAAG	GAGGCGTAGG	AGTCGCGCAG
9241	CTTGTTGACC	AGCTCGGCGG	TGACCTGCAC	GTCTAGGGCG	CAGTAGTCCA	GGGTTTCCTT
9301	GATGATGTCA	TACTTATCCT	GTCCCTTTTT	TTTCCACAGC	TGCGCGTTGA	GGACAAACTC
9361	TTCCGGGTCT	TTCCAGTACT	CTTGGATCGG	AAACCCGTCG	GCCTCCGAAC	GGTAAGAGCC
9421	TAGCATGTAG	AACTGGTTGA	CGGCCTGGTA	GCGCGAGCAT	CCCTTTTCTA	CGGGTAGCGC
9481	GTATGCCTGC	GCGGCCTTCC	GGAGCGAGGT	GTGGGTGAGC	GCAAAGGTGT	CCCTAACCAT
9541	GACTTTGAGG	TACTGGTATT	TGAAGTCACT	GTGCTCGCAT	CCGCCCTGCT	CCCAGAGCAA
9601	AAAGTCGGTG	CGCTTTTGGG	AACGCGGGTT	TGGCAGGGCG	AAGGTGACAT	CGTTGAAAAG
9661	TATCTTTCCC	GCGCGAGGCA	TAAAGTTGCG	TGTGATGCGG	AAGGGTCCCG	GCACCTCGGA
9721	ACGGTTGTTA	ATTACCTGGG	CGGCGAGCAC	GATCTCGTCG	AAGCCGTIGA	TGTTGTGGCC
9781	CACGATGTAA	AGTTCCAAGA	AGCGCGGGGT	GCCCTTGATG	GAGGGCAATT	TTTTAAGTTC
9841	CTCGTAGGTG	AGCTCCTCAG	GGGAGCTGAG	CCCGTGTCT	GACAGGGCCC	AGTCTGCAAG
9901	ATGAGCGGTTG	GAAGCGAOGA	ATGAGCTCCA	CAGGTCAACG	GCCATTAGCA	TTTGCAAGTG
9961	GTCCGGAAG	GTCTTAAACT	GCGCGACCTAT	GGCCATTTTT	TCTGGGTGA	TGCAGTAGAA
10021	GGTAAGCGGG	TCTTGTTCCC	AGCGTCCCCA	TCCAAGGTCC	ACGGCTAGGT	CTCGCGGGGC
10081	GGTCACCAGA	GGCTCATCTC	CGCCGAACTT	CATAACCAGC	ATGAAGGGCA	CGAGCTGCTT
10141	CCCAAAGGCC	CCCATCCAAG	TATAGGTCTC	TACATCGTAG	GTGACAAAGA	GACGCTCGGT
10201	GCGAGGATGC	GAGCCGATCG	GGAGAAGCTG	GATCTCCCGC	CACCACTTGG	AGGAGTGGCT
10261	GTTGATGTGG	TGAAAGTAGA	AGTCCCTGCG	ACGGGCCGAA	CACCTGTCGT	GGCTTTTGTA
10321	AAAACGTGCG	CAGTACTGGC	AGCGGTGCAC	GGGCTGTACA	TCCTGCACGA	GGTTGACCTG
10381	ACGACCGCGC	ACAAGGAAGC	AGAGTGGGAA	TTTGAGCCCC	TGCGCTGGCG	GGTTTGCGTG
10441	GTGGTCTTCT	ACTTCGGCTG	CTTGTCCTTG	ACCGTCTGOC	TGCTCGAGGG	GAGTTATGGT
10501	GGATCGGACC	ACCACGCCCC	GCGAGCCCCA	AGTCCAGATG	TCCGCGCGCG	GCGGTGCGAG
10561	CTTGATGACA	ACATCGCGCA	GATGGGAGCT	GTCCATGCTC	TGGAGCTCCC	GCGGOGACAG
10621	GTCAGGCGGG	AGCTCCTGCA	GGTTTACCTC	GCATAGCCGG	GTGAGGCGCG	GCGCTAGGTC
10681	CAGGTGATAC	CTGATTTCCT	GCGGCTGGTT	GGTGGCGGCG	TCGATGACTT	GCAAGAGGCC
10741	GCATCCCCGC	GGCGCGACTA	CGGTACCGCG	CGGCGGGCGG	TGGGCCGCGG	GGGTGTCCTT
10801	GGATGATGCA	TCTAAAAGCG	GTGACGCGGG	CGGGCCCCCG	GAGGTAGGGG	GGGCTCGGGA
10861	CCCGCCGGGA	GAGGGGGCAG	GGGCACGTCG	GCGCCGCGCG	CGGGCAGGAG	CTGGTGCTGC
10921	GCGCGGAGGT	TGCTGGCGAA	CGCGACGACG	CGGCGGTTGA	TCTCCTGAAT	CTGGCGCCTC
10981	TGCGTGAAGA	CGACGGGCCC	GGTGAGCTTG	AACCTGAAAG	AGAGTTTCGAC	AGAATCAATT
11041	TCCGTGTGCT	TGACGGCGGC	CTGGCGCAAA	ATCTCCTGCA	CGTCTCCTGA	GTTGTCTTGA
11101	TAGGCGATTT	CGGCCATGAA	CTGCTCGATC	TCTTCTCCT	GGAGATCTCC	GCGTCCGGCT
11161	CGCTCCACGG	TGGCGGCGAG	GTGCTTGGAG	ATGCGGGCCA	TGAGCTGCGA	GAAGGCGTTG
11221	AGGCCTCCCT	CGTTCCAGAC	GCGGCTGTAG	ACCACGCCCC	CTTCGGCATC	GCGGGCGCGC
11281	ATGACCACCT	GCGCGAGATT	GAGCTCCACG	TGCGGGGCGA	AGACGGCGTA	GTTCGCGAGG
11341	CGCTGAAAGA	GGTAGTTGAG	GGTGGTGGCG	GTGTGTTCTG	CCACGAAGAA	GTACATAACC
11401	CAGCGTCCGA	ACGTGGATTG	GTTGATATCC	CCCAAGGCCT	CAAGGCGCTC	CATGGCCTCG
11461	TAGAAGTCCA	CGGCGAAGTT	GAAAAACTGG	GAGTTGCGCG	CCGACACGGT	TAACCTCTCC
11521	TCCAGAAGAC	GGATGAGCTC	GCGGACAGTG	TGCGGCACCT	CGCGCTCAAA	GGCTACAGGG
11581	GCCTCTTCTT	CTTCAATCTC	CTCTTCCATA	AGGGCCTCCC	CTTCTTCTTC	TTCTTCTGGC
11641	GCGCGTGGGG	GAGGGGGGAC	ACGGCGGGCA	CGACGGCGCA	CCGGGAGGCG	GTGACAAAG
11701	CGCTCGATCA	TCTCCCCGCG	GCGACGGCGC	ATGGTCTCGG	TGACGGCGCG	GCCGTTCTCG
11761	CGGGGGCGCA	GTTGGAAGAC	GCCGCCCGTC	ATGTCCCGGT	TATGGGTTGG	CGGGGGGCTG
11821	CCGTGCGGCA	GGGATACGGC	GCTAACGATG	CATCTCAACA	ATTGTTGTGT	AGGTACTCCG
11881	CCACCGAGGG	ACCTGAGCGA	GTCCGCATCG	ACCGGATCGG	AAAACCTCTC	GAGAAAGGCG
11941	TCTAACCAGT	CACAGTCCGA	AGGTAGGCTG	AGCACGCTGG	CGGGCGGCGG	CGGGTGGCGG
12001	TGCGGGTTGT	TTCTGGCGGA	GGTGCTGCTG	ATGATGTAAT	TAAAGTAGGC	GGTCTTGAGA
12061	CGGCGGATGG	TGACAGAAG	CACCATGTCC	TTGGGTCCGG	CCTGCTGAAT	GCGCAGGCGG

Nucleotide Sequence Analysis (cont.)

12121	TCGGCCATGC	CCCAGGCTTC	GTTTGTGACAT	CGGCGCAGGT	CTTTGTAGTA	GTCTTGCATG
12181	AGCCTTTCTA	CCGGCACTTC	TTCTTCTCCT	TCCTCTTGTC	CTGCATCTCT	TGCATCTATC
12241	GCTACGGCGG	CGGCGGAGTT	TGGCCGTAGG	TGGCGCCCTC	TTCTTCCCAT	GCGTGTGACC
12301	CCGAAGCCCC	TCATCGGCTG	AAGCAGGGCC	AGGTCGGOGA	CAAOCGCGTC	GGCTAATATG
12361	GCCTGCTGCA	CCTGCGTGAG	GGTAGACTGG	AAGTCATCCA	TGTCCACAAA	GCGGTGGTAT
12421	GCGCCCGTGT	TGATGGTGTA	AGTGCAGTTG	GCCATAACGG	ACCAGTTAAC	GGTCTGGTGA
12481	CCCGGCTGCG	AGAGCTCGGT	GTACCTGAGA	CGCGAGTAAG	CCCTTGAGTC	AAAGACGTAG
12541	TCGTTGCAAG	TCCGCACCAG	GTACTGATAT	CCCACCAAAA	AGTGCGGCGG	CGGCTGGCGG
12601	TAGAGGGGCC	AGCGTAGGGT	GGCCGGGGCT	COGGGGGCGA	GGTCTTCCAA	CATAAGGCGA
12661	TGATATCCGT	AGATGTACCT	GGATGATCCAG	GTGATGCCGG	CGGCGGTGGT	GGAGGCGCGC
12721	GGAAAGTCGC	GGACGCGGTT	CCAGATGTTG	CGCAGCGGCA	AAAAGTGCTC	CATGGTCCGG
12781	ACGCTCTGGC	CGGTGAGGCG	TGCGCAGTCG	TTGACGCTCT	AGACCGTGCA	AAAGGAGAGC
12841	CTGTAAGCGG	GCACTCTTCC	GTGGTCTGGT	GGATAAATTC	GCAAGGGTAT	CATGGCGGAC
12901	GACCGGGGTT	CGAACCCCGG	ATCCGGCCGT	CCGCGGTGAT	CCATGCGGTT	ACCGCCCGCG
12961	TGTCGAACCC	AGGTGTGCGA	CGTCAGACAA	CGGGGGAGCG	CTCCTTTTGG	CTTCCTTCCA
13021	GGCGGGCGGG	CTGCTGCGCT	AGCTTTTTTG	GCCACTGGCC	GCGCGCGGCG	TAAGCGGTTA
13081	GGCTGGAAAG	CGAAAGCATT	AAAGTGCTCG	CTCCCTGTAG	CCGGAGGGTT	ATTTTCCAAG
13141	GGTTGAGTCG	CAGGACCCCC	GGTTCGAGTC	TCGGGCGCGC	CGGACTGCGG	CGAACGGGGG
13201	TTTGCCCTCCC	CGTCATGCAA	GACCCCGCTT	GCAAATTCCT	CCGGAACAG	GGACGAGCCC
13261	CTTTTTTGCT	TTTCCCAGAT	GCATCCGGTG	CTGCGGCAGA	TGCGCCCCCC	TCCTCAGCAG
13321	CGGCAAGAGC	AAGAGCAGCG	GCAGACATGC	AGGGCACCCT	CCCCCTCTCC	TACCGCGTCA
13381	GGAGGGGCAA	CATCCGCGGC	TGACGCGCGC	GCAGATGGTG	ATTACGAACC	CCCGGGCGGC
13441	CGGGCCCGGC	ACTACCTGGA	CTTGGAGGAG	GGCGAGGGCC	TGGCGCGGCT	AGGAGCGCCC
13501	TCTCTGAGC	GACACCCAAG	GGTGCAGCTG	AAGCGTGACA	CGCGCGAGGC	GTACGTGCGG
13561	CGGCAGAACC	TGTTTTCGGA	CCGCGAGGGA	GAGGAGCCCG	AGGAGATGCG	GGATCGAAAG
13621	TTCCACGCAG	GGCGCGAGTT	GCGGCATGGC	CTGAACCGCG	AGCGGTTGCT	GCGCGAGGAG
13681	GACTTTGAGC	CCGACGCGCG	GACCGGGATT	AGTCCCGCGC	GCGCACAGT	GCGCGCCGCG
13741	GACCTGGTAA	CCGCGTACGA	GCAGACGGTG	AACCAGGAGA	TTAACTTTCA	AAAAAGCTTT
13801	AACAACCAAG	TGCGCACGCT	TGCGCGCGCG	GAGGAGGTGG	CTATAGGACT	GATGCATCTG
13861	TGGGACTTTG	TAAGCGCGCT	GGAGCAAAC	CCAAATAGCA	AGCCGCTCAT	GGCGCAGCTG
13921	TTCTTTATAG	TGCAGCACAG	CAGGACAAC	GAGGCATTCA	GGGATGCGCT	GCTAAACATA
13981	GTAGAGCCCG	AGGGCGCGTG	GCTGCTCGAT	TTGATAAACA	TTCTGCAGAG	CATAGTGGTG
14041	CAGGAGCGCA	GCTTGAGCCT	GGCTGACAAG	GTGGCCGCCA	TTAACTATT	CATGCTCAGT
14101	CTGGGCAAGT	TTTACGCCCC	CAAGATATAC	CATACCCCTT	ACGTTCCCAT	AGACAAGGAG
14161	GTAAAGATCG	AGGGGTTCTA	CATGCGCATG	GCGTTGAAGG	TGCTTACCTT	GAGCGACGAC
14221	CTGGGCGTTT	ATCGCAACGA	GCGCATCCAC	AAGGCCGTGA	GCGTGAGCCG	GCGGCGCGAG
14281	CTCAGCGACC	GCGAGCTGAT	GCACAGCCTG	CAAAGGGCCC	TGGCTGCGAC	GGGCAGCGGC
14341	GATAGAGAGG	CCGAGTCCTA	CTTTGACGCG	GGCGCTGACC	TGCGCTGGGC	CCCAAGCCGA
14401	CGCGCCCTGG	AGGCAGCTGG	GGCCGGACCT	GGGCTGGCGG	TGGCACCCCG	GCGCGCTGGC
14461	AACGTCGGCG	GCGTGGAGGA	ATATGACGAG	GACGATGAGT	ACGAGCCAGA	GGACGGCGAG
14521	TACTAAGCGG	TGATGTTTCT	GATCAGATGA	TGCAAGACGC	AACGGACCCG	GCGGTGCGGG
14581	CGGCGCTGCA	GAGCCAGCCG	TCCGGCCTTA	ACTCCACGGA	CGACTGGCGC	CAGGTATGCG
14641	ACCGCATCAT	GTCGCTGACT	GCGCGTAACC	CTGACGCGTT	CCGGCAGCAG	CCGCAGGCCA
14701	ACCGGCTCTC	CGCAATTCTG	GAAGCGGTGG	TCCCGGCGCG	CGCAAACCCC	ACGCACGAGA
14761	AGGTGCTGGC	GATCGTAAAC	GCGCTGGCCG	AAAACAGGGC	CATCCGGCCC	GATGAGGCCG
14821	GCTTGGTCTA	CGACGCGCTG	CTTCAGCGCG	TGGCTCGTTA	CAACAGCGGC	CAACGTGCAGA
14881	CCAACCTGGA	CCGGCTGGTG	GGGGATGTGC	GCGAGGCCGT	GGCGCAGCGT	GAGCGCGCGC
14941	AGCAGCAGGG	CAACCTGGGC	TCCATGTGTTG	CACTAAACGC	CTTCCTGAGT	ACACAGCCCC
15001	CCAACGTGCC	GCGGGGACAG	GAGGACTACA	CCAACTTTGT	GAGCGCACTG	CGGCTAATGG
15061	TGACTGAGAC	ACCGCAAAGT	GAGGTGTACC	AGTCCGGGCC	AGACTATTTT	TTCCAGACCA
15121	GTAGACAAGG	CCTGCAGACC	GTAACCTGTA	GCCAGGCTTT	CAAGAACTTG	CAGGGGCTGT
15181	GGGGGGTGCG	GGCTCCCAAC	GCGGACCGCG	CGACCGTGTC	TAGCTTGCTG	ACGCCCAACT
15241	CGCGCCTGTT	GCTGCTGCTA	ATAGCGCCCT	TCAOGGACAG	TGGCAGCGTG	TCCCGGGACA
15301	CATACCTAGG	TCACTTGCTG	ACACTGTACC	GCGAGGCCAT	AGGTCAGGCG	CATGTGGACG
15361	AGCATACTTT	CCAGGAGATT	ACAAGTGTCA	GCCGCGCGCT	GGGCGAGGAG	GACACGGGCA
15421	GCCTGGAGGC	AACCTGGAAC	TACCTGCTGA	CCAACCGGCG	GCAGAAGATC	CCCTCGTTGC
15481	ACAGTTTAAA	CAGCGAGGAG	GAGCGCATCT	TGCGCTATGT	GCAGCAGAGC	GTGAGCCTTA

Nucleotide Sequence Analysis (cont.)

15541	ACCTGATGCG	CGACGGGGTA	ACGCCCCAGCG	TGGCGCTGGA	CATGACCGCG	CGCAACATGG
15601	AACCGGGCAT	GTATGCCTCA	AACCGGCCGT	TTATCAATCG	CCTAATGGAC	TACTTGCATC
15661	GCGCGGCGCG	CGTGAACCCC	GAGTATTTCA	CCAATGCCAT	CTTGAACCOG	CACTGGCTAC
15721	CGCCCCCTGG	TTTCTACACC	GGGGGATTTG	AGGTGCCCCG	GGGTAACGAT	GGATTCCCTCT
15781	GGGACGACAT	AGACGACAGC	GTGTTTTCCC	CGCAACCGCA	GACCCTGCTA	GAGTTGCAAC
15841	AGCGCGAGCA	GGCAGAGGCG	GCGCTGCGAA	AGGAAAGCTT	CCGCAGGGCA	AGCAGCTTGT
15901	CGATCTAGG	CGCTGCGGCC	CGCGGTCAG	ATGCGAGTAG	CCCATTTCCA	AGCTTGATAG
15961	GGTCTTTTAC	CAGCACTCGC	ACCACCCGCC	CGCGCTGCT	GGGCGAGGAG	GAGTACCTAA
16021	ACAACTCGCT	GCTGCAGCG	CAGCGCGAAA	AGAACCTGCC	TCCGGCATTT	CCCAACAACG
16081	GGATAGAGAG	CCTAGTGGAC	AAGATGAGTA	GATGGAAGAC	GTATGCGCAG	GAGCACAGGG
16141	ATGTGCCCGG	CCCGCGCCCG	CCCACCCGTC	GTCAAAGGCA	CGACCGTCAG	CGGGGCTCGG
16201	TGTGGGAGGA	CGATGACTCG	GCAGACGACA	GCAGCGTCC	GGATTTGGGA	GGGAGTGGCA
16261	ACCCGTTTGC	GCACCTTCGC	CCCAGGCTGG	GGAGAATGTT	TTAAAAAAA	AAAAAAAAG
16321	CATGATGCAA	AATAAAAAAC	TCACCAAGGC	CATGGCACCG	AGCGTTGGTT	TTCTTGATT
16381	CCCCTTAGTA	TGCAGCGCGC	GGCGATGTAT	GAGGAAGGTC	CTCCTCCCTC	CTACGAGAGC
16441	CTGGTGAGCG	CGGCGCCAGT	GGCGCGCGCG	CTGGGTTCCC	CCTTCGATGC	TCCCCCTGGAC
16501	CCGCGGTTTG	TGCCTCCGCG	GTACCTGCGG	CCTACCGGGG	GGAGAAACAG	CATCOGTTAC
16561	TCTGAGTTGG	CACCCCTATT	CGACACCACC	CGTGTGTACC	TTGTGGACAA	CAAGTCAACG
16621	GATGTGGCAT	CCCTGAACTA	CCAGAACGAC	CACAGCAACT	TTCTAACCCAC	GGCATTTCAA
16681	AACAATGACT	ACAGCCCGGG	GGAGGCAAGC	ACACAGACCA	TCAATCTTGA	CGACCGTTCC
16741	CCTGCGGGCG	GCGACCTGAA	AACCATCCTG	CATACCAACA	TGCCAAATGT	GAACGAGTTC
16801	ATGTTTACCA	ATAAGTTTAA	GGCGCGGGTG	ATGGTGTGCG	GCTCGCTTAC	TAAGGACAAA
16861	CAGGTGGAGC	TGAAATATGA	GTGGGTGGAG	TTACGCTGCG	CCGAGGGCAA	CTACTCCGAG
16921	ACCATGACCA	TAGACCTTAT	GAACAACGCG	ATCGTGGAGC	ACTACTTGAA	AGTGGGCGAG
16981	CAGAACGGGG	TTCTGGAAAG	CGACATCGGG	GTAAAGTTTG	ACACCCGCAA	CTTCAGACTG
17041	GGGTTTGACC	CAGTCACTGG	TCTTGTCATG	CCTGGGGTAT	ATACAAACGA	AGCTTCCAT
17101	CCAGACATCA	TTTTGCTGCC	AGGATCGCGG	GTGGACTTCA	CCCACAGCCG	CCTGAGCAAC
17161	TTGTTGGGCA	TCCGCAAGCG	GCAACCCCTC	CAGGAGGGCT	TTAGGATCAC	CTACGATGAC
17221	CTGGAGGGTG	GTAACATTCC	CGCACTGTTG	GATGTGGACG	CCTACCAGGC	AAGCTTAAAA
17281	GATGACACCG	AACAGGGCGG	GGATGGCGCA	GGCGGCGGCA	ACAACAGTGG	CAGCGGCGCG
17341	GAAGAGAACT	CCAACGCGGC	AGCCGCGGCA	ATGCAGCCGG	TGGAGGACAT	GAACGATCAT
17401	GCCATTGCGG	GCGACACCTT	TGCCACACGG	GCGGAGGAGA	AGCGCGCTGA	GGCCGAGGCA
17461	GCGGCAGAAG	CTGCCGCCCC	CGCTGGGCAA	CCCGAGGTCG	AGAAGCCTCA	GAAGAAACCG
17521	GTGATCAAAC	CCCTGACAGA	CCACAGCAAG	AAACGCAGTT	ACAACCTAAT	AAGCAATGAC
17581	AGCACCTTCA	CCCAGTACCG	CAGCTGGTAC	CTTGCAATCA	ACTACGGGGA	CCCTCAGACC
17641	GGGATCGGCT	CATGGACCC	CCTTTGCACT	CCTGACGTAA	CCTGCGGCTC	GGAGCAGGTC
17701	TACTGGTGGT	TGCCAGACAT	GATGCAAGAC	CCCGTGACCT	TCCGCTCCAC	GAGCCAGATC
17761	AGCAACTTTC	CGGTGGTGGG	CGCCGAGCTG	TTGCCCGTGC	ACTCCAAGAG	CTTCTACAAC
17821	GACCAGGCGG	TCTACTCCCA	GCTCATCCGC	CAGTTTACCT	CTCTGACCCA	CGTGTTCAT
17881	CGCTTTCCCG	AGAACCAGAT	TTTGGCGCGC	CCGCCAGCCC	CCACCATCAC	CACCGTCAGT
17941	GAAAACGTTT	CTGCTCTCAC	AGATCACGGG	ACGCTACCGC	TGCGCAACAG	CATCGGAGGA
18001	GTCCAGCGAG	TGACCATTAC	TGACGCCAGA	CGCCGCACCT	GCCCCCTACG	TTACAAGGCC
18061	CTGGGCATAG	TCTCGCCGCG	CGTCCTATCG	AGCCGCACCT	TTTGAGCAAA	CATGTCCATC
18121	CTTATATCGC	CCAGCAATAA	CACAGGCTGG	GGCCTGCGCT	TCCCAAGCAA	GATGTTTGGC
18181	GGGGCAAAGA	AGCGCTCCGA	CCAACACCCA	GTGCGCGTGC	GCGGGCACTA	CCCGCGCGCC
18241	TGGGGCGCGC	ACAA ² CGGG	CGCACTGGG	CGCACCACCG	TCGATGACGC	CATTGACGCG
18301	GTGGTGGAGG	AGGCGCGCAA	CTACACGCC	ACGCCGCCAC	CAGTGTCCAC	AGTGGACGCG
18361	GCCATTGAGA	CCGTGGTGGG	CGGAGCCCGG	CGTTATGCTA	AAATGAAGAG	ACGCGCGGAG
18421	CGCGTAGCAC	GTCGCCACCG	CCGCCGACCC	GGCACTGCGG	CCCAACGCGC	GGCGGCGGCC
18481	CTGCTTAACC	GCGCACGTCG	CACCGGCCGA	CGGGCGGCCA	TGCGGGCCGC	TGCAAGGCTG
18541	GCCGCGGGTA	TTGTCACTGT	GCCCCCAGG	TCCAGGCGAC	GAGCGGCCGC	CCGACGAGCC
18601	GCGGCCATTA	GTGCTATGAC	TCAGGCTCGC	AGGGGCAACG	TGTACTGGGT	GCGCGACTCG
18661	GTTAGCGGCC	TGCGCGTGCC	CGTGCGCACC	CGCCCCCGCG	GCAACTAGAT	TGCAAGAAAA
18721	AACTACTTAG	ACTCGTACTG	TTGTATGTAT	CCAGCGGCGG	CGGCGCGCAA	CGAAGCTATG
18781	TCCAAGCGCA	AAATCAAAGA	AGAGATGCTC	CAGGTCATCG	CGCCGGAGAT	CTATGGCCCC
18841	CCGAAGAAGG	AAGAGCAGGA	TTACAAGCCC	CGAAAGCTAA	AGCGGCTCAA	AAAGAAAAAG
18901	AAAGATGATG	ATGATGATGA	ACTTGACGAC	GAGGTGGAAC	TGCTGCACGC	AACCGCGCCC

Nucleotide Sequence Analysis (cont.)

18961	AGGCGGCGGG	TACAGTGGAA	AGGTCGACGC	GTAAGACGTG	TTTTGCGACC	CGGCACCACC
19021	GTAGTTTTTA	CGCCCGGTGA	GCGCTCCACC	CGCACCTACA	AGCGCGTGT	TGATGAGGTG
19081	TACGGCGACG	AGGACCTGCT	TGAGCAGGCC	AACGAGCGCC	TGGGGAGT	TGCCTACCGA
19141	AAGCGGCATA	AGGACATGTT	GGGTTGCCG	CTGGACGAGG	GCAACCCAAC	ACTTAGCCTA
19201	AAGCCCGTGA	CACTGCAGCA	GGTGTGCCC	ACGCTTGAC	CGTCCGAAGA	AAAGCGGGC
19261	CTAAAGCGCG	AGTCTGGTGA	CTTGGCACCC	ACCGTGCAGC	TGATGGTACC	CAAGCGCCAG
19321	CGACTGGAAG	ATGTCCTTGA	AAAAATGACC	GTGGAGCCTG	GGCTGGAGCC	CGAGGTCCGC
19381	GTGCGGCCAA	TCAAGCAGGT	GGCACCGGGA	CTGGGCGTGC	AGACCGTGA	CGTTTCAGATA
19441	CCCACCACCA	GTAGCACTAG	TATTGCCACT	GCCACAGAGG	GCATGGAGAC	ACAAACGTCC
19501	CGGTTGCCT	CGGCGGTGGC	AGATGCCGCG	GTGCAGGCGG	CGCTGCGGCG	CGCGTCCAAA
19561	ACCTCTACGG	AGGTGCAAAAC	GGACCCGTGG	ATGTTTCGCG	TTTCAGCCCC	CCGGCGCCCC
19621	CGCCGTTCOA	GGAAGTACGG	CACCGCCAGC	GCATACTGCG	CCGAATATGC	CCTACATCCT
19681	TCCATCGCGC	CTACCCCGCG	CTATCGTGGC	TACACCTACC	GCCCCAGAAG	ACGAGCGACT
19741	ACCCGACGCC	GAACCAACCAC	TGGAACCCGCG	CGCGCGCTG	GCCGTGCGCA	GCCCCGTGCTG
19801	GGCCGATTT	CGGTGCGCAG	GGTGGCTCGC	GAAGGAGGCA	GGACCTGTGT	GCTGCCAACA
19861	GCGCGCTACC	ACCCAGCAT	CGTTTAAAG	CGGTCCTTG	TGGTCTCTGC	AGATATGGCC
19921	CTCACCTGCC	GCCTCCGTTT	CCGGTGCCG	GGATTCCGAG	GAAGAATGCA	CGGTAGGAGG
19981	GGCATGGCCG	GCCACGGCCT	GACGGGCGGC	ATGCGTCTGT	CGCACCACCG	CGCGGGCGGC
20041	GCGTGCACCC	GTCGCATGCG	CGGCGGTATC	CTGCCCCCTC	TTATTCCTACT	GATCGCGCGG
20101	GCGATTGGCG	CCGTGCCCGG	AAATGCATCC	GTGGCCTTGC	AGGCGCAGAG	ACACTGATTA
20161	AAAACAAGTT	GCATGTGGAA	AAATCAAAAT	AAAAAGTCTG	GAGTCTCAGC	CTCGCTTGTT
20221	CTGTAACTA	TTTTGTAGAA	TGGAAGACAT	CAACTTTGCG	TCTCTGGCCC	CGCGACACCG
20281	CTCGCGCCCG	TTCATGGGAA	ACTGGCAAGA	TATCGGCACC	AGCAATATGA	GCGGTGGCGC
20341	CTTCAGCTGG	GGCTCGCTGT	GGAGCGGCAT	TAAAAATTTT	GTTCCACCA	TAAAGAACTA
20401	TGGCAGCAAG	GCCTGGAACA	GCAGCACAGG	CCAGATGCTG	AGGGACAAGT	TGAAAGAGCA
20461	AAATTTCCAA	CAAAAGGTGG	TAGATGGCCT	GGCCTCTGGC	ATTAGCGGGG	TGGTGGACCT
20521	GGCCAACCA	GCAGTGCAAA	ATAAGATTAA	CAGTAAGCTT	GATCCCCGCC	CTCCCGTAGA
20581	GGAGCCCTCA	CCGGCCGTGG	AGACAGTGTG	TCCAGAGGGG	CGTGGCGAAA	AGCGTCCCGG
20641	CCCGACAGG	GAAGAACTC	TGGTGAACGA	AATAGATGAG	CCTCCCTCGT	ACGAGGAGGC
20701	ACTAAAGCAA	GGCCTGCCCA	CCACCCGTCC	CATCGCGCCC	ATGGGTACCG	GAGTGTCTGG
20761	CCAGCACACA	CCTGTAAACG	TGGACCTGCC	TCCCCCGGCT	GACACCCAGC	AGAAACCTGT
20821	GCTGCCAGGG	CCGTCCGCGG	TTGTTGTAA	CGCCCTTAGC	CGCGCGTCCC	TGCGCCGTGC
20881	CGCCAGCGGT	CCGCGATCGA	TGCGGCCCGT	AGCCAGTGGC	AACTGGCAAA	GCACACTGAA
20941	CAGCATCGTG	GGTCTGGGGG	TGCAATCCCT	GAAGCGCCGA	CGATGCTTCT	AAATAGCTAA
21001	CGTGTCTGAT	GTGTCTATGA	TGCGTCCATG	TGCGCGCCAG	AGGAGCTGCT	GAGCCGCGCT
21061	GCGCCCGCTT	TCCAAGATGG	CTACCCCTTC	GATGATGCCG	CAGTGGTCTT	ACATGCACAT
21121	CTCGGGCCAG	GACGCTTCGG	AGTACCTGAG	CCCCGGGCTG	GTGCAGTTTG	CCCAGGCCAC
21181	CGAGACGTAC	TTCAGCCTGA	ATAACAAGTT	TAGAAACCCC	ACGGTGGCAC	CTAGCCACGA
21241	CGTAACCACA	GACCGGTCCC	AGCGTTTGAC	GCTGCGGTTT	ATCCCTGTGG	ACCGCGAGGA
21301	TACCGCGTAC	TCGTACAAAG	CGCGTTTCAC	CCTGGCTGTG	GGTGACAACC	GTGTGCTTGA
21361	TATGGCTTCC	ACGTACTTTG	ACATCCGCGG	CGTGCTGGAC	AGGGGGCCTA	CTTTTAAGCC
21421	CTACTCCGGC	ACTGCCTACA	ACGCTCTAGC	TCCCAAGGGC	GCTCCTAACT	CCTGTGAGTG
21481	GGAACAAACC	GAAGATAGCG	GCCGGGCAGT	TGCCGAGGAT	GAAGAAGAGG	AAGATGAAGA
21541	TGAAGAAGAG	GAAGAAGAAG	AGCAAAACGC	TGAGATCAG	GCTACTAAGA	AAACACATGT
21601	CTATGCCCCAG	GCTCCTTTGT	CTGGAGAAAC	AATTACAAAA	AGCGGGCTAC	AAATAGGATC
21661	AGACAATGCA	GAAACACAAG	CTAAACCTGT	ATACGCAGAT	CCTTCCTATC	AACCAGAACC
21721	TCAAATTTGGC	GAATCTCAGT	GGAAACGAAGC	TGATGCTAAT	GCGGCAGGAG	GGAGAGTGCT
21781	TAAAAAAACA	ACTCCCATGA	AACCATGCTA	TGGATCTTAT	GCCAGGCCTA	CAAATCCTTT
21841	TGGTGGTCAA	TCCGTTCTGG	TTCCGGATGA	AAAAGGGGTG	CCTCTTCCAA	AGGTTGACTT
21901	GCAATTCTTC	TCAAATACTA	CCTCTTTGAA	CGACCGGCA	GGCAATGCTA	CTAAACCAAA
21961	AGTGGTTTTG	TACAGTGAAG	ATGTAATAT	GGAAACCCCA	GACACACATC	TGTCTTACAA
22021	ACCTGAAAA	GGTGATGAAA	ATTCTAAAGC	TATGTTGGGT	CAACAATCTA	TGCCAAACAG
22081	ACCCAATTAC	ATTGCTTTCA	GGGACAATTT	TATTGGCCTA	ATGTATTATA	ACAGCACTGG
22141	CAACATGGGT	GTTCTTGCTG	GTCAGGCATC	GCAGCTAAAT	GCCGTGGTAG	ATTGCAAGA
22201	CAGAAACACA	GAGCTGTCTT	ATCAACTCTT	GCTTGATTCC	ATAGGTGATA	GAACCAGATA
22261	TTTTTCTATG	TGGAATCAGG	CTGTAGACAG	CTATGATCCA	GATGTTAGAA	TCATTGAAAA
22321	CCATGGAAC	GAGGATGAAT	TGCCAAATTA	TTGTTTCTCT	CTTGGGGGTA	TGGGGGTAAC

Nucleotide Sequence Analysis (cont.)

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22381 TGACACCTAT CAAGCTATTA AGGCTAATGG CAATGGCTCA GCGATAATG GAGATACTAC
22441 ATGGACAAAA GATGAAACTT TTGCAACACG TAATGAAATA GGAGTGGGTA ACAACTTTGC
22501 CATGGAAATT AACCTAAATG CCAACCTATG GAGAAATTTT CTTTACTCCA ATATTGOGCT
22561 GTACCTGCTA GACAAGCTAA AATACAACCC CACCAATGTG GAAATATCTG ACAAACCCAA
22621 CACCTACGAC TACATGAACA AGCGAGTGGT GGCTCCCGGG CTTGTAGACT GCTACATTAA
22681 CCTTGGGGCG CGCTGGTCTC TGGACTACAT GGACAACGTT AATCCCTTTA ACCACCACOG
22741 CAATGOGGGC CTCCGTTATC GCTCCATGTT GTTGGGAAAC GCGCGCTACG TGCCCTTTCA
22801 CATTGAGGTG CCCCAAAAGT TTTTGGCCAT TAAAAACCTC CTCCTCTGCG CAGGCTCATA
22861 TACATATGAA TGGAACCTCA GGAAGGATGT TAACATGGTT CTGCAGAGCT CTCTGGGAAA
22921 CGATCTTAGA GTTGACGGGG CTAGCATTAA GTTTGACAGC ATTTGTCTTT ACGCCACCTT
22981 CTTCCCCATG GCCCACAACA CGGCCTCCAC GCTGGAAGCC ATGCTCAGAA ATGACACCAA
23041 CGACCAGTCC TTTAATGACT ACCTTTCCGC CGCCAACATG CTATACCCCA TACCCGCCAA
23101 CGCCACCAAC GTGCCCATCT CCATCCCATC GCGCAACTGG GCAGCATTTG CGGTTGGGC
23161 CTTACACGCG TTGAAGACAA AGGAAACCCC TTCCCTGGGA TCAGGCTACG ACCCTTACTA
23221 CACCTACTCT GGCTCCATAC CATACCTTGA TCCCAACCTC TATCTTAAATC ACACCTTTAA
23281 GAAGGTGGCC ATTACCTTTG ACTCTTCTGT TAGCTGGCCG GGCAACGACC GCCTGCTTAC
23341 TCCCAATGAG TTTGAGATTA AACGCTCAGT TGACGGGGAG GGCTACAACG TAGCTCAGTG
23401 CAACATGACC AAGGACTGGT TCCTGGTGCA GATGTTGGCC AACTACAATA TTGGCTACCA
23461 GGGCTTCTAC ATTCCAGAAA GCTACAAGGA CCGCATGTAC TCGTTCCTTA GAAACTTCCA
23521 GCCCATGAGC CGGCAAGTGG TTGACGATAC TAAATACAAG GAGTATCAGC AGGTTGGAAT
23581 TCTTCACCAG CATAACAAC TGCCTACCTC ACTAATAGGC AAAACOGCGG TTGACAGTAT
23641 ACAGGCTTAC CCCGCCAAGC GCGATCGCAC CCTTTGGCGC ATCCCATTTCT CCAGTAACTT
23701 TACCCAGAAA AAGTTTCTTT GCGATCGCAC CCAAACCTTT CTCTACGCCA ACTCCGCCCA
23761 TATGTCCATG GGCGCACTCA CAGACCTGGG CATGGACGAG CCCACCCCTC TTTATGTTTT
23821 CGCGCTAGAC ATGACTTTTG AGGTGGATCC CCAGCCGCAC CGCGCGGTCA CGGAGACCGT
23881 GTTTGAAGTC TTTGACGTGG TCCGTGTGCA CCAGCCGCAC TAAAAGAAGC AAGCAACATC
23941 GTACCTGCGC ACGCCCTTCT CGGCCGGCAA CGCCACAACA AAAGCCATG TCAAAGATCT
24001 AACACAGCT GCCGCCATGG GCTCCAGTGA AGCAGAACTG AAGCCATG TTTCCAGGCT
24061 TGGTTGTGGG CCATATTTTT TGGGCACCTA TGACAAGCGC TTTCCAGGCT TTGTTTCTCC
24121 ACACAAGCTC GCCTGCGCCA TAGTCAATAC GGCCGGTGGC GAGACTGGGG GCGTACACTG
24181 GATGGCCTTT GCCTGGAACC CGCGTCAAAA AACATGCTAC CTCTTTGAGC CTTTGGCTT
24241 TTCTGACCAA CGACTCAAGC AGGTTTACCA GTTTGAGTAC GAGTCACTCC TGCGCCGTAG
24301 CGCCATTGCT TCTTCCCCCG ACCGCTGTAT AACGCTGGAA AAGTCCACCC AAAGCGTGCA
24361 GGGGCCCAAC TCGGCCGCCT GTGGACTATT CTGCTGCATG TTTCTCCACG CTTTGGCCAA
24421 CTGGCCCCAA ACTCCCATGG ATCACAACCC CACCATGAAC CTTATTACCG GGTACCCAA
24481 CTCCATGCTT AACAGTCCCC AGGTACAGCC CACCCTGCGT CGCAACCAGG AACAGCTCTA
24541 CAGCTTCTCT GAGCGCCACT CGCCCTACTT CCGCAGCCAC AGTGCGCAGA TTAGGAGCGC
24601 CACTTCTTTT TGTCACCTGA AAAACATGTA AAAATAATGT ACTAGGAGAC ACTTTCAATA
24661 AAGGCAAATG TTTTATTATT TACACTCTCG GGTGATTATT TACCCCCAC CTTGCGCTC
24721 TGCGCGGTTT AAAAATCAAA GGGGTTCTGC AGTGTCTCAC TTAACCTCAG GCACAACCAT CCGCGCAGC
24781 ACGTTGCGAT ACTGGTGTAT AGTGCTCCAC CAGGCTGCGC ACCATCACCA ACGCGTTTAG CAGGTGGGGC
24841 TCGGTGAAGT TTTCACTCCA GGTGGGGCCT CCGCCCTGCG CGCGCGAGTT GCGATACACA
24901 GCCGATATCT TGAAGTCGCA GTTGGGGCCT GGGTGGTGCA CGCTGGCCAG CACGCTCTTG
24961 GGGTTGCAGC ACTGGAACAC TATCAGCGCC GCGTTGCTCA GGGCGAACGG AGTCAACTTT
25021 TCGGAGATCA GATCCGCGTC CAGGTCCTCC GCGTTGCTCA AGTTCAGCTC GCACCGTAGT
25081 GGTAAGCTTCT TTCCCAAAAA GGGTGCATCG CCGGCTCTGG GCGTTAGGAT ACAGCGCCTG CATGAAAGCC
25141 GGCATCAGAA GGTGACCGTG CCGGCTCTGG GCGCTTCTAG AGAAGAACAT GCCGCAAGAC
25201 TTGATCTGCT TAAAAGCCAC CTGAGCCTTT GCGTCATGCA CGCAGCACCT TCGGTGGGTG
25261 TTGCGGAAA ACTGATTGGC CGGACAGGCC CCGTCTTCTA CGATCTTGGC CTTGCTAGAC
25321 TTGGAGATCT GCACCACATT CCGGCCCCAC CCGTCTTCTA CCGTCTTGGC CCGTCTTGGC
25381 TGCTCCTTCA GCGCGCGCTG CCGGTTTTCT GTGTAGACAC TTAAGCTCGC CTTGCTATCT AGCGCAGCGG
25441 TTATTTATCA TAATGCTCCC GTGTAGACAC TTAAGCTCGC CTTGCTATCT AGCGCAGCGG
25501 TGCAGCCACA ACGCGCAGCC CCGGCCCCAT CCGGCTCTGG TGGTGCTTGT AGGTACCTTC TGCAAACGAC
25561 TGCAGGTACG CCTGCAAGGA TCGGCCCCAT ATCGTCACAA AGGTCTTGGT GCTGGTGAAG
25621 GTCAGCTGCA ACCCGCGGTG CTCCTCGTTT AGCCAGGTCT TGCATACGGC CGCCAGAGCT
25681 TCCACTTGGT CAGGCAGTAG CTTGAAGTTT GCCTTTAGAT CGTTATCCAC GTGGTACTTG
25741 TCCATCAACG CGCGCGCAGC CTCCATGCCC TTCTCCCACG CAGACACGAT CGGCAGGCTC

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Nucleotide Sequence Analysis (cont.)

25801	AGCGGGTTTA	TCACCGTGCT	TTCACCTTTC	GCTTCACTGG	ACTCTTCCTT	TTCCTCTTGC
25861	GTCCGCATAC	CCCGCGCCAC	TGGGTCTGCT	TCATTCAGCC	GCCGCACCGT	GCGCTTACCT
25921	CCCTTGCCGT	GCTTGATTAG	CACCGGTGGG	TGCTGAAAC	CCACCATTTG	TAGCGCCACA
25981	CTTCTCTTTT	CTTCTCTGCT	GTCCACGATC	ACCTCTGGGG	ATGGCGGGCG	CTCGGGCTTG
26041	GGAGAGGGGC	GCTTCTTTTT	CTTTTTGGAC	GCAATGGCCA	AATCOGCCGT	CGAGGTCCAT
26101	GGCGCGGGGC	TGGGTGTGCG	CGGCACCAGC	GCATCTTGTC	ACGAGTCTTC	TTCGTCTCTG
26161	GACTCGAGAC	GCCGCCTCAG	CCGCTTTTTT	GGGGGCGCGC	GGGGAGGCGG	CGGCGACGGC
26221	GACGCGGACG	ACACGTCTCT	CATGCTTGGT	GGACGTGCGG	COGCACCGCG	TCCGCGCTCG
26281	GGGGTGGTTT	CGCGCTGCTC	CTCTTCCCGA	CTGGCCATTT	CCTTCTCTTA	TAGGCAGAAA
26341	AAGATCATGG	AGTCAGTCGA	GAAGGAGGAC	AGCCTAACCG	CCCCCTTTGA	GTTCGCCACC
26401	ACCGCCTCCA	CCGATGCCGC	CAACGCGCCT	ACCACCTTCC	CCGTCGAGGC	ACCCCGCGTT
26461	GAGGAGGAGG	AAGTGATTAT	CGAGCAGGAC	CCAGGTTTTG	TAAGCGAAGA	CGACGAGGAT
26521	CGCTCAGTAC	CAACAGAGGA	TAAAAAGCAA	GACCAGGACG	ACGCAGAGGC	AAACGAGGAA
26581	CAAGTCGGGC	GGGGGGACCA	AAGGCATGGC	GACTACCTAG	ATGTGGGAGA	CGACGTGCTG
26641	TTGAAGCATC	TGCAGCGCCA	GTGCGCCATT	ATCTGCGACG	CGTTGCAAGA	GCGCAGCGAT
26701	GTGCCCCCTG	CCATAGCGGA	TGTCAGCCCT	GCCTACGAAC	GCCACCTGTT	GCCACCGCGC
26761	CCCGCCCCCA	AACGCCAAGA	AAACGGCACA	TGCGAGCCCA	ACCCGCGCCT	CAACTTCTAC
26821	CCCGTATTTG	CCGTGCCAGA	GGTGCTTGCC	ACCTATCACA	TCTTTTTTCCA	AAACTGCAAG
26881	ATACCCCTAT	CCTGCGGTGC	CAACCGCAGC	CGAGCGGACA	AGCAGCTGGC	CTTGCGGCAG
26941	GGCGCTGTCA	TACCTGATAT	CGCCTCGCTC	GACGAAGTGC	CAAAAATCTT	TGAGGGTCTT
27001	GGACGCGACG	AGAAAACGCG	GGCAAACGCT	CTGCAACAAG	AAAACAGCGA	AAATGAAAAGT
27061	CACGTGTGAG	TGCTGGTGGA	ACTTGAGGGT	GACAACGCGC	GCCTAGCCGT	GCTGAAAACG
27121	AGCATCGAGG	TCACCCACTT	TGCCTACCGG	GCACCTAAC	TACCCCCCAA	GGTTATGAGC
27181	ACAGTCATGA	GCGAGCTGAT	CGTGCGCCGT	GCACGACCCC	TGGAGAGGGA	TGCAAACTTG
27241	CAAGAACAAA	CCGAGGAGGG	CCTACCCGCA	GTTGGCGATG	AGCAGCTGGC	GCGCTGGCTT
27301	GAGAOGCGCG	AGCCTGCCGA	CTTGAGGAG	CGAOGCAAGC	TAATGATGGC	CGCAGTGCTT
27361	GTTACCGTGG	AGCTTGAGTG	CATGCAGCGG	TTCTTTGCTG	ACCCGGAGAT	GCAGCGCAAG
27421	CTAGAGGAAA	CGTTGCACTA	CACCTTTCCG	CAGGGCTACG	TGCGCCAGGC	CTGCAAAATT
27481	TCCAACGTGG	AGCTCTGCAA	CCTGGTCTCC	TACCTTGGA	TTTTGCACGA	AAACCGCCTC
27541	GGGCAAAACG	TGCTTTCATT	CACGCTCAAG	GGCGAGGCGC	GCCGCGACTA	CGTCCGCGAC
27601	TGCGTTTACT	TATTTCTGTG	CTACACCTGG	CAAAACGGCCA	TGGGCGTGTG	GCAGCAATGC
27661	CTGGAGGAGC	GCAACCTAAA	GGAGCTGCAG	AAGCTGCTAA	AGCAAAACTT	GAAGGACCTA
27721	TGGACGGCCT	TCAACGAGCG	CTCCGTGGCC	GCGCACCTGG	CGGACATTAT	CTTCCCGGAA
27781	CGCCTGCTTA	AAACCCTGCA	ACAGGGTCTG	CCAGACTTCA	CCAGTCAAAG	CATGTTGCAA
27841	AACCTTAGGA	ACTTTATCCT	AGAGCGTTCA	GGAAATCTGC	CCGCCACCTG	CTGTCCGCTT
27901	CCTAGCGACT	TTGTGCCCAT	TAAGTACCGT	GAATGCCCTC	CGCCGCTTTG	GCGTCACTGC
27961	TACCTTCTGC	AGCTAGCCAA	CTACCTTGCC	TACCACTCCG	ACATCATGGA	AGACGTGAGC
28021	GGTGACGGCC	TACTGGAGTG	TCACTGTCCG	TGCAACCTAT	GCACCCCGCA	CCGCTCCCTG
28081	GTCTGCAATT	CGCAACTGCT	TAGCGAAAAGT	CAAATTATCG	GTACCTTTGA	GCTGCAGGGT
28141	CCCTCGCCTG	ACGAAAAGTC	CGCGGCTCCG	GGGTGAAAC	TCACTCCGGG	GCTGTGGACC
28201	TGGGCTTACC	TTCGCAAATT	TGTACCTGAG	GACTACCACG	CCCACGAGAT	TAGGTTCTAC
28261	GAAGACCAAT	CCCGCCCGCC	AAATGCCGAG	CTTACCGCCT	GCGTCATTAC	CCAGGGCCAC
28321	ATCCTTGGCC	AATTGCAAGC	CATCAACAAA	GCCCCCAAG	AGTTTCTGCT	ACGAAAGGGA
28381	CGGGGGGTTT	ACCTGGACCC	CCAGTCCGCG	GAGGAGCTCA	ACCCAATCCC	CCCGCCGCGG
28441	CAGCCCTATC	AGCAGCCGCG	GGCCCTTGCT	TCCCAGGATG	GCACCCAAAA	AGAAGCTGCA
28501	GCTGCGGCGG	CCGCEACCCA	CGGACGAGGA	GGAAATACTG	GACAGTCAGG	CAGAGGAGGT
28561	TTTGGAACGAG	GAGGAGGAGA	TGATGGAAGA	CTGGGACACC	CTAGACGAAG	CTTCCGAGGC
28621	CGAAGAGGTG	TCAGACGAAA	CACCGTCACC	CTCGGTCCGA	TTCCCTCTCG	CGGCGCCCCA
28681	GAAATTGGCA	ACCGTTCCCA	GCATGGCTAC	AACCTCCGCT	CCTCAGGCGC	CGCCGGCACT
28741	CCCTGTTCCG	CGACCCAACC	GTAGGATGGG	CACCACTGGA	ACCAGGGCCG	GTAAGTCTAA
28801	GCAGCCGCGG	CCGTTAGCCC	AAGAGCAACA	ACAGCGQCAA	GGCTACCGCT	CGTGGCGCGG
28861	GCACAAGAAC	GCCATAGTTG	CTTGCTTGCA	AGACTGTGGG	GGCAACATCT	CCTTCGCCCC
28921	CCGCTTTCTT	CTCTACCATC	ACGGCGTGCC	CTTCCCCCGT	AACATCCTGC	ATTACTACCG
28981	TCATCTCTAC	AGCCCCTACT	GCACCGGCGG	CAGCGGCAGC	GCAGCAACA	GCAGCGGTCA
29041	CACAGAAGCA	AAGGCGACCG	GATAGCAAGA	CTCTGACAAA	GCCCAAGAAA	TCCACAGCGG
29101	CGGCAGCAGC	AGGAGGAGGA	GCGCTGCGTC	TGGCGCCCAA	CGAACCCGTA	TCGACCCGCG
29161	AGCTTAGAAA	TAGGATTTTT	CCCCTCTGCT	ATGCTATATT	TCAACAAAGC	AGGGGCCAAG

Nucleotide Sequence Analysis (cont.)

29221	AACAAGAGCT	GAAAAATAAAA	AACAGGTCTC	TGCGCTCCCT	CACCCGCAGC	TGCCTGTATC
29281	ACAAAAGCGA	AGATCAGCTT	CGGCGCAOCG	TGGAAGACGC	GGAGGCTCTC	TTCAGCAAAT
29341	ACTGCGCGCT	GA CTCTTAAG	GA CTAGTTTC	GCGCCCTTTC	TCAAATTTAA	GCGCGAAAAAC
29401	TACGTCATCT	CCAGCGGCCA	CACCOGGGCG	CAGCACCTGT	CGTCAGCGCC	ATTATGAGCA
29461	AGGAAATTCC	CACGCCCTAC	ATGTGGAGTT	ACCAGCCACA	AATGGGACTT	GCGGCTGGAG
29521	CTGCCCAAGA	CTACTCAACC	CGAATAAACT	ACATGAGCGC	GGGACCCAC	ATGATATCCC
29581	GGGTCAACGG	AATCCGCGCC	CACOGAAACC	GAATTCTCCT	CGAACAGGCG	GCTATTACCA
29641	CCACACCTCG	TAATAACCTT	AATCCCCGTA	GTTGGCCCGC	TGCCCTGGTG	TACCAGGAAA
29701	GTCCCGCTCC	CACCACTGTG	GTACTTCCCA	GAGACGCCCA	GGCCGAAGTT	CAGATGACTA
29761	ACTCAGGGGC	GCAGCTTGCG	GGCGGCTTTC	GTACAGGGT	GCGGTGCGCC	GCGCAGGGTA
29821	TAACTCACCT	GAAAAATCAGA	GGGCGAGGTA	TTCAGCTCAA	CGACGAGTCG	GTGAGCTCCT
29881	CTCTTGGTCT	CCGTCCGGAC	CGGACATTTT	AGATCGGCGG	CGCTGGCCGC	TCTTCATTTA
29941	CGCCCCGTCA	GGCGATCCTA	ACTCTGCAGA	CCTCGTCTTC	GGAGCCGGGC	TCCGGAGGCA
30001	TTGGAACCTC	ACAATTTATT	GAGGAGTTTG	TGCCTTCGGT	TTACTTCAAC	CCCTTTTCTG
30061	GACCTCCCGG	CCACTACCCG	GACCAGTTTA	TTCCCAACTT	TGACGCGGTG	AAAGACTCGG
30121	CGGACGGCTA	CGACTGAATG	ACCAGTGGAG	AGGCAGAGCG	ACTGCGCCTG	ACACACCTCG
30181	ACCACTGCCG	CCGCCACAAG	TGCTTTGCCC	GCGGCTCCGG	TGAGTTTGTG	TAGTTTGAAT
30241	TGCCCGAAGA	GCATATCGAG	GGCCCGGGCG	ACGGCGTCCG	GCTCACCACC	CAGGTAGAGC
30301	TTACACGTAG	CCTGATTCCG	GAGTTTACCA	AGCGCCCCCT	GCTAGTGGAG	CGGGAGCGGG
30361	GTCCCTGTGT	TCTGACCGTG	GTTTGCAACT	GTCTTAACCC	TGGATTACAT	CAAGATCTTT
30421	GTTGTCATCT	CTGTGCTGAG	TATAATAAAT	ACAGAAATTA	GAATCTACTG	GGGCTCCTGT
30481	CGCCATCCTG	TGAACGCCAC	CGTTTTTACC	CACCCAAAGC	AGACCAAAGC	AAACCTCACC
30541	TCGGTTTTCG	ACAAGCGGGC	CAATAAGTAC	CTTACCTGGT	ACTTAAACGG	CTCTTCAATT
30601	GTAATTTACA	ACAGTTTCCA	GCGAGACGAA	GTAAGTTTGC	CACACAACCT	TCTCGGCTTC
30661	AACTACACCG	TCAAGAAAAA	CACCACCACC	ACCACCCTCC	TCACCTGCCG	GGAACGTAAG
30721	AGTGCGTCAC	CGGTTGCTGC	CGCCACACCT	ACAGCCTGAG	CGTAACCAGA	CATTACTCCC
30781	ATTTTTTCAA	AACAGGAGGT	GAGCTCAACT	CCCGGAATC	AGGTCAAAAA	AGCATTTTGC
30841	GGGGTGCTGG	GATTTTTTAA	TTAAGTATAT	GAGCAATTCA	AGTAACTCTA	CAAGCTTGTC
30901	TAATTTTTCT	GGAAATGGGG	TCCGGGTTAT	CCTTACTCTT	GTAATTCGTG	TTATTCTTAT
30961	ACTAGCACTT	CTGTGCCCTTA	GGGTGCGCG	CTGCTGCACG	CACGTTTGTA	CCTATTGTCA
31021	GCTTTTTTAA	CGCTGGGGGC	AACATCCAAG	ATGAGGTACA	TGATTTTAGG	CTTGCTCGCC
31081	CTTGCGGCAG	TCTGCAGCGC	TGCCAAAAAG	GTTGAGTTTA	AGGAACCAGC	TTGCAATGTT
31141	ACATTTAAAT	CAGAAGCTAA	TGAATGCACT	ACTCTTATAA	AATGCACCAC	AGAACATGAA
31201	AAGCTTATTA	TTGCCACAA	AGACAAAATT	GGCAAGTATG	CTGTATATGC	TATTTGGCAG
31261	CCAGGTGACA	CTAACGACTA	TAATGTCACA	GTCTTCCAAG	GTGAAAATCG	TAAAACTTTT
31321	ATGTATAAAT	TTCCATTTTTA	TGAAATGTGC	GATATTACCA	TGTACATGAG	CAAAACGTAC
31381	AAGTTGTGGC	CCCCACAAAA	GTGTTTAGAG	AACACTGGCA	CCTTTTGTTC	CACCGCTCTG
31441	CTTATTACAG	CGCTTGCTTT	CGTATGTACC	TTACTTTATC	TCAAATACAA	AAGCAGACGC
31501	AGTTTTATTG	ATGAAAAGAA	AATGCCTTGA	TTTTCCGCTT	GCTTGTATTG	CCCTGGACAA
31561	TTTACTCTAT	GTGGGATATG	CTCCAGGCGG	GCAAGATTAT	ACCCACAACC	TTCAAATCAA
31621	ACTTTCCTGG	ACGTTAGCGC	CTGATTTCTG	CCAGCGCCTG	CACTGCAAA	TTGATCAAA
31681	CCAGCTTCAG	CTTGCCCTGCT	CCAGAGATGA	COGGCTCAAC	CATCGCGCCC	ACAACGGACT
31741	ATCGCAACAC	CACTGCTACC	GGACTAACAT	CTGCCCTAAA	TTTACCCCAA	GTTTCATGCC
31801	TTGTCAATGA	CTGGGCGAGC	TTGGACATGT	GGTGGTTTTC	CATAGCGCTT	ATGTTTGTTC
31861	GCCTTATTAT	TATGTGGCTT	ATTTGTTGCC	TAAAGCGCAG	ACGCGCCAGA	CCCCCATCT
31921	ATAGGCCTAT	CATTGTGCTC	AACCCACACA	ATGAAAAAAT	TCATAGATTG	GACGGTCTGA
31981	AACCATGTTT	TCTTCTTTTA	CAGTATGATT	AAATGAGACA	TGATTCCTCG	AGTTCTTATA
32041	TTATTGACCC	TTGTTGCGCT	TTTCTGTGCG	TGCTCTACAT	TGGCCGCGGT	CGCTCACATC
32101	GAAGTAGATT	GCATCCCAAC	TTTCACAGTT	TACCTGCTTT	ACGGATTGTG	CACCCCTATC
32161	CTCATCTGCA	GCCTCGTCAC	TGTAGTCATC	GCCTTCATTC	AGTTCAATTGA	CTGGGTTTGT
32221	GTGCGCATTG	CGTACCTCAG	GCACCATCCG	CAATACAGAG	ACAGGACTAT	AGCTGATCTT
32281	CTCAGAATTC	TTTAATTATG	AAACGGAGTG	TCATTTTGTG	TTTGCTGATT	TTTTCGCCCC
32341	TACCTGTGCT	TTGCTCCCAA	ACCTCAGCGC	CTCCCAAAAG	ACATATTTCC	TGCAGATTCA
32401	CTCAAATATG	GAACATTCCC	AGCTGCTACA	ACAAACAGAG	CGATTTGTCA	CGAGCCTGGT
32461	TATACGCCAT	CATCTCTGTC	ATGGTTTTTT	GCAGTACCAT	TTTTGCCCTA	GCCATATATC
32521	CATACCTTGA	CATTGGCTGG	AATGCCATAG	ATGCCATGAA	CCACCCTACT	TTCCCACTGC
32581	CCGCTGTGCT	ACCACTGCAA	CAGGTTATTG	CCCCAATCAA	TCAGCCTGCG	CCCCCTTCTC

Nucleotide Sequence Analysis (cont.)

32641	CCACCCCCAC	TGAGATTAGC	TACTTTAATT	TGACAGGTGG	AGATGACTGA	ATCTCTAGAT
32701	CTAGAATTGG	ATGGAATTAA	CACCGAACAG	CGCCTACTAG	AAAGGCGCAA	GGCGGCGTCC
32761	GAGCGAGAAC	GCCTAAAACA	AGAAGTTGAA	GACATGGTTA	ACCTACACCA	GTGTAAAAGA
32821	GGTATCTTTT	GTGTGGTCAA	GCAGGCCAAA	CTTACCTACG	AAAAAACCCAC	TACCGGCAAC
32881	CGCCTCAGCT	ACAAGCTACC	CACCCAGGCG	CAAAAACTGG	TGCTTATGGT	GGGAGAAAAA
32941	CCTATCACCG	TCACCCAGCA	CTCGGCAGAA	ACAGAGGGCT	GCCTGCACTT	CCCCTATCAG
33001	GGTCCAGAGG	ACCTCTGCAC	TCTTATTAAA	ACCATGTGTG	GTATTAGAGA	TCTTATTCCA
33061	TTCAACTAAC	ATAAACACAC	AATAAATTAC	TTACTTAAAA	TCAGTCAGCA	AATCTTTGTC
33121	CAGCTTATTC	AGCATCACCT	CCTTTCCTTC	CTCCCAACTC	TGGTATCTCA	GCCGCTTTT
33181	AGCTGCAAAC	TTTCTCCAAA	GTTTAAATGG	GATGTCAAAT	TCCTCATGTT	CTGTGCCCTC
33241	CGCACCCACT	ATCTTCATAT	TGTTGCAGAT	GAAACGCGCC	AGACCGTCTG	AGACACCTT
33301	CAACCCCGTG	TATCCATATG	ACACAGAAAC	CGGGCCTCCA	ACTGTGCCCT	TTCTTACCCC
33361	TCCATTTGTT	TCACCCCAATG	GTTTCCAAGA	AAGTCCCCCT	GGAGTTCTCT	CTCTAOGCGT
33421	CTCCGAACCT	TTGGACACCT	CCCACGGCAT	GCTTGGGCTT	AAAATGGGCA	GCGGTCTTAC
33481	CCTAGACAAG	GCCGGAAACC	TCACCTCCCA	AAATGTAACC	ACTGTTACTC	AGCCACTTAA
33541	AAAAACAAAG	TCAAACATAA	GTTTGGACAC	CTCCGCACCA	CTTACAATTA	CCTCAGGCGC
33601	CCTAACAGTG	GCAACCACCG	CTCCTCTGAT	AGTTACTAGC	GGCGCTCTTA	GCGTACAGTC
33661	ACAAGCCCCA	CTGACCGTGC	AAGACTCCAA	ACTAAGCATT	GCTACTAAAG	GGCCCATTTAC
33721	AGTGTGAGAT	GGAAAGCTAG	CCCTGCAAA	ATCAGCCCCC	CTCTCTGGCA	GTGACAGCGA
33781	CACCCCTTACT	GTAACCTGCAT	CACCCCGCT	AACTACTGCC	ACGGGTAGCT	TGGGCATTAA
33841	CATGGAAGAT	CCTATTTATG	TAAATAATGG	AAAAATAGGA	ATTAAAATAA	GCGGTCCTTT
33901	GCAAGTAGCA	CAAAACTCCG	ATACACTAAC	AGTAGTTACT	GGACCAGGTG	TCACCGTTGA
33961	ACAAAACTCC	CTTAGAACCA	AAGTTGCAGG	AGCTATTGGT	TATGATTTCAT	CAAACAACAT
34021	GGAAATTAAA	ACGGGCGGTG	GCATGCGTAT	AAATAACAAC	TTGTTAATT	TAGATGTGGA
34081	TTACCCATTT	GATGCTCAAA	CAAAACTACG	TCTTAAACTG	GGGCAGGGAC	CCCTGTATAT
34141	TAATGCATCT	CATAACTTGG	CATAAACTA	TAACAGAGGC	CTATACCTTT	TTAATGCATC
34201	AAACAATACT	AAAAAACTGG	AAGTTAGCAT	AAAAAAATCC	AGTGGACTAA	ACTTTGATAA
34261	TACTGCCATA	GCTATAAATG	CAGGAAAGGG	TCTGGAGTTT	GATACAAACA	CATCTGAGTC
34321	TCCAGATATC	AACCCAATAA	AAACTAAAAT	TGGCTCTGGC	ATTGATTACA	ATGAAAAOCC
34381	TGCCATGATT	ACTAAACTTG	GAGCGGGTTT	AAGCTTTGAC	AACTCAGGGG	CCATTACAAT
34441	AGGAAACAAA	AATGATGACA	AACTTACCCT	GTGGACAACC	CCAGACCCAT	CTCCTAAGTC
34501	CAGAATTTCAT	TCAGATAATG	ACTGCAAATT	TACTTTGGTT	CTTACAAAAT	GTGGGAGTCA
34561	AGTACTAGCT	ACTGTAGCTG	CTTTGGCTGT	ATCTGGAGAT	CTTTCATCCA	TGACAGGCAC
34621	CGTTGCAAGT	GTTAGTATAT	TCCTTAGATT	TGACCAAAAC	GGTGTTCATA	TGGAGAACTC
34681	CTCACTTAAA	AAACATTACT	GGAACCTTAG	AAATGGGAAC	TCAACTAATG	CAAATCCATA
34741	CACAAATGCA	GTTGGATTMTA	TGCCTAACCT	TCTAGCCTAT	CCAAAAACCC	AAAGTCAAAC
34801	TGCTAAAAAT	AACATTGTCA	GTCAAGTTTA	CTTGCATGGT	GATAAACTA	AACCTAGAT
34861	ACTTACCATT	ACACTTAATG	GCCTAGTGA	ATCCACAGAA	ACTAGCGAGG	TAAGCACTTA
34921	CTCTATGTCT	TTTACATGGT	CCTGGGAAAG	TGGAAAATAC	ACCACTGAAA	CTTTTGCTAC
34981	CAACTCTTAC	ACCTTCTCCT	ACATTGCCCA	GGAATAAAGA	ATCGTGAACC	TGTTGCATGT
35041	TATGTTTCAA	CGTGGGATCC	TTTATTATAG	GGGAAGTCCA	CGCCTACATG	GGGGTAGAGT
35101	CATAATCGTG	CATCAGGATA	GGGCGGTGGT	GCTGCAGCAG	CGCGCGAATA	AACTGCTGCC
35161	GCGCGCGCTC	CGTCCTGCAG	GAATACAACA	TGGCAGTGGT	CTCCTCAGCG	ATGATTGCGA
35221	CCGCCCCGAG	CATGAGACGC	CTTGTCTCTC	GGGCACAGCA	GCGCACCCCTG	ATCTCACTTA
35281	AATCAGCACA	GTAACCTGCAG	CACAGCACCA	CAATATTGTT	CAAAATCCCA	CAGTGCAAGG
35341	CGCTGTATCC	AAAGCTCATG	GCGGGGACCA	CAGAACCCAC	GTGGCCATCA	TACCACAAGC
35401	GCAGGTAGAT	TAAGTGGCGA	CCCCTCATAA	ACACGCTGGA	CATAAACATT	ACCTCTTTTG
35461	GCATGTTGTA	ATTCAACCACC	TCCCGGTACC	ATATAAACCT	CTGATTAAAC	ATGGCGCCAT
35521	CCACCACCAT	CCTAAACCAG	CTGGCCAAAA	CCTGCCCGCC	GGCTATGCAC	TGCAGGGAAC
35581	CGGGACTGGA	ACAATGACAG	TGGAGAGGCC	AGGACTCGTA	ACCATGGATC	ATCATGCTCG
35641	TCATGATATC	AATGTTGGCA	CAACACAGGC	ACACGTGCAT	ACACTTCCTC	AGGATTACAA
35701	GCTCCTCCCG	CGTCAGAACCC	ATATCCAGG	GAACAACCCA	TTCTGAAATC	AGCGTAAATC
35761	CCACACTGCA	GGGAAGACCT	CGCACGTAAC	TCACGTTGTG	CATTGTCAAA	GTGTTACATT
35821	CGGGCAGCAG	CGGATGATCC	TCCAGTATGG	TAGCGCGGGT	CTCTGTCTCA	AAAGGAGGTA
35881	GGCGATCCCT	ACTGTACGGA	GTGCGCCGAG	ACAACCGAGA	TCGTGTTGGT	CGTAGTGTCA
35941	TGCCAAATGG	AACGCCCGAG	GTAGTCATAT	TTCATCGACA	CGGCACCAGC	TCAATCAGTC
36001	ACAGTGTAAG	AAGGGCCAAG	TACAGGCGGA	GTATATATAG	GACTAAAAAA	TGACGTAACC

Nucleotide Sequence Analysis (cont.)

36061 GTTAAAGTCC AAAAAAACA CCCAGAAAAC CGCACGCGAA CCTACGCCCA GAAACGAAAG
36121 CAAAAAACC CACAACTTCC TCAARTCTTC ACTTCCGTTT TCCCACGATA CGTCACTTCC
36181 CATTTTAAAA AAAC TACAAT TCCCAATACA TGCAAGTTAC TCCGCCCTAA AACCTACGTC
36241 ACCCGCCCCG TTCCCACGCC CCGCGCCACG TCACAAACTC CACCCCTCA TTATCATATT
36301 GGCTTCAATC CAAAATAAGG TATATTATGA TGATG

//

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANTS: Gregory, R.J., Armentano, D., Couture, L.A., Smith,
A.E.

10

(ii) TITLE OF INVENTION: GENE THERAPY FOR CYSTIC FIBROSIS

(iii) NUMBER OF SEQUENCES: 9

15

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: LAHIVE & COCKFIELD
- (B) STREET: 60 STATE STREET, SUITE 510
- (C) CITY: BOSTON
- (D) STATE: MASSACHUSETTS
- (E) COUNTRY: USA
- (F) ZIP: 02109

20

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: ASCII

25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE: 02-DEC-1993
- (C) CLASSIFICATION:

30

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/985,478
- (B) FILING DATE: 02-DEC-1992
- (C) CLASSIFICATION:

35

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Hanley, Elizabeth A.
- (B) REGISTRATION NUMBER: 33,505
- (C) REFERENCE/DOCKET NUMBER: NZI-014CP2PC

40

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (617) 227-7400
- (B) TELEFAX: (617) 227-5941

45

(2) INFORMATION FOR SEQ ID NO:1:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 133..4572

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10	AATTGGAAGC AAATGACATC ACAGCAGGTC AGAGAAAAAG GGTGAGCGG CAGGCACCCA	60
	GAGTAGTAGG TCTTTGGCAT TAGGAGCTTG AGCCCAGACG GCCCTAGCAG GGACCCCAGC	120
	GCCCGAGAGA CC ATG CAG AGG TCG CCT CTG GAA AAG GCC AGC GTT GTC	168
15	Met Gln Arg Ser Pro Leu Glu Lys Ala Ser Val Val	
	1 5 10	
	TCC AAA CTT TTT TTC AGC TGG ACC AGA CCA ATT TTG AGG AAA GGA TAC	216
	Ser Lys Leu Phe Phe Ser Trp Thr Arg Pro Ile Leu Arg Lys Gly Tyr	
	15 20 25	
20	AGA CAG CGC CTG GAA TTG TCA GAC ATA TAC CAA ATC CCT TCT GTT GAT	264
	Arg Gln Arg Leu Glu Leu Ser Asp Ile Tyr Gln Ile Pro Ser Val Asp	
	30 35 40	
25	TCT GCT GAC AAT CTA TCT GAA AAA TTG GAA AGA GAA TGG GAT AGA GAG	312
	Ser Ala Asp Asn Leu Ser Glu Lys Leu Glu Arg Glu Trp Asp Arg Glu	
	45 50 55 60	
30	CTG GCT TCA AAG AAA AAT CCT AAA CTC ATT AAT GCC CTT CGG CGA TGT	360
	Leu Ala Ser Lys Lys Asn Pro Lys Leu Ile Asn Ala Leu Arg Arg Cys	
	65 70 75	
35	TTT TTC TGG AGA TTT ATG TTC TAT GGA ATC TTT TTA TAT TTA GGG GAA	408
	Phe Phe Trp Arg Phe Met Phe Tyr Gly Ile Phe Leu Tyr Leu Gly Glu	
	80 85 90	
	GTC ACC AAA GCA GTA CAG CCT CTC TTA CTG GGA AGA ATC ATA GCT TCC	456
	Val Thr Lys Ala Val Gln Pro Leu Leu Leu Gly Arg Ile Ile Ala Ser	
	95 100 105	
40	TAT GAC CCG GAT AAC AAG GAG GAA CGC TCT ATC GCG ATT TAT CTA GGC	504
	Tyr Asp Pro Asp Asn Lys Glu Glu Arg Ser Ile Ala Ile Tyr Leu Gly	
	110 115 120	
45	ATA GGC TTA TGC CTT CTC TTT ATT GTG AGG ACA CTG CTC CTA CAC CCA	552
	Ile Gly Leu Cys Leu Leu Phe Ile Val Arg Thr Leu Leu Leu His Pro	
	125 130 135 140	
50	GCC ATT TTT GGC CTT CAT CAC ATT GGA ATG CAG ATG AGA ATA GCT ATG	600
	Ala Ile Phe Gly Leu His His Ile Gly Met Gln Met Arg Ile Ala Met	
	145 150 155	
55	TTT AGT TTG ATT TAT AAG AAG ACT TTA AAG CTG TCA AGC CGT GTT CTA	648
	Phe Ser Leu Ile Tyr Lys Lys Thr Leu Lys Leu Ser Ser Arg Val Leu	
	160 165 170	

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	GAT AAA ATA AGT ATT GGA CAA CTT GTT AGT CTC CTT TCC AAC AAC CTG	696
	Asp Lys Ile Ser Ile Gly Gln Leu Val Ser Leu Leu Ser Asn Asn Leu	
	175 180 185	
5	AAC AAA TTT GAT GAA GGA CTT GCA TTG GCA CAT TTC GTG TGG ATC GCT	744
	Asn Lys Phe Asp Glu Gly Leu Ala Leu Ala His Phe Val Trp Ile Ala	
	190 195 200	
10	CCT TTG CAA GTG GCA CTC CTC ATG GGG CTA ATC TGG GAG TTG TTA CAG	792
	Pro Leu Gln Val Ala Leu Leu Met Gly Leu Ile Trp Glu Leu Leu Gln	
	205 210 215 220	
15	GCG TCT GCC TTC TGT GGA CTT GGT TTC CTG ATA GTC CTT GCC CTT TTT	840
	Ala Ser Ala Phe Cys Gly Leu Gly Phe Leu Ile Val Leu Ala Leu Phe	
	225 230 235	
20	CAG GCT GGG CTA GGG AGA ATG ATG ATG AAG TAC AGA GAT CAG AGA GCT	888
	Gln Ala Gly Leu Gly Arg Met Met Met Lys Tyr Arg Asp Gln Arg Ala	
	240 245 250	
25	GGG AAG ATC AGT GAA AGA CTT GTG ATT ACC TCA GAA ATG ATT GAA AAT	936
	Gly Lys Ile Ser Glu Arg Leu Val Ile Thr Ser Glu Met Ile Glu Asn	
	255 260 265	
30	ATC CAA TCT GTT AAG GCA TAC TGC TGG GAA GAA GCA ATG GAA AAA ATG	984
	Ile Gln Ser Val Lys Ala Tyr Cys Trp Glu Glu Ala Met Glu Lys Met	
	270 275 280	
35	TAT GTG AGA TAC TTC AAT AGC TCA GCC TTC TTC TTC TCA GGG TTC TTT	1080
	Tyr Val Arg Tyr Phe Asn Ser Ser Ala Phe Phe Phe Ser Gly Phe Phe	
	305 310 315	
40	GTG GTG TTT TTA TCT GTG CTT CCC TAT GCA CTA ATC AAA GGA ATC ATC	1128
	Val Val Phe Leu Ser Val Leu Pro Tyr Ala Leu Ile Lys Gly Ile Ile	
	320 325 330	
45	CTC CGG AAA ATA TTC ACC ACC ATC TCA TTC TGC ATT GTT CTG CGC ATG	1176
	Leu Arg Lys Ile Phe Thr Thr Ile Ser Phe Cys Ile Val Leu Arg Met	
	335 340 345	
50	GCG GTC ACT CGG CAA TTT CCC TGG GCT GTA CAA ACA TGG TAT GAC TCT	1224
	Ala Val Thr Arg Gln Phe Pro Trp Ala Val Gln Thr Trp Tyr Asp Ser	
	350 355 360	
55	CTT GGA GCA ATA AAC AAA ATA CAG GAT TTC TTA CAA AAG CAA GAA TAT	1272
	Leu Gly Ala Ile Asn Lys Ile Gln Asp Phe Leu Gln Lys Gln Glu Tyr	
	365 370 375 380	
55	AAG ACA TTG GAA TAT AAC TTA ACG ACT ACA GAA GTA GTG ATG GAG AAT	1320
	Lys Thr Leu Glu Tyr Asn Leu Thr Thr Thr Glu Val Val Met Glu Asn	
	385 390 395	

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	GTA	ACA	GCC	TTC	TGG	GAG	GAG	GGA	TTT	GGG	GAA	TTA	TTT	GAG	AAA	GCA	1368
	Val	Thr	Ala	Phe	Trp	Glu	Glu	Gly	Phe	Gly	Glu	Leu	Phe	Glu	Lys	Ala	
				400					405					410			
5	AAA	CAA	AAC	AAT	AAC	AAT	AGA	AAA	ACT	TCT	AAT	GGT	GAT	GAC	AGC	CTC	1416
	Lys	Gln	Asn	Asn	Asn	Asn	Arg	Lys	Thr	Ser	Asn	Gly	Asp	Asp	Ser	Leu	
			415					420					425				
10	TTC	TTC	AGT	AAT	TTC	TCA	CTT	CTT	GGT	ACT	CCT	GTC	CTG	AAA	GAT	ATT	1464
	Phe	Phe	Ser	Asn	Phe	Ser	Leu	Leu	Gly	Thr	Pro	Val	Leu	Lys	Asp	Ile	
			430				435						440				
15	AAT	TTC	AAG	ATA	GAA	AGA	GGA	CAG	TTG	TTG	GCG	GTT	GCT	GGA	TCC	ACT	1512
	Asn	Phe	Lys	Ile	Glu	Arg	Gly	Gln	Leu	Leu	Ala	Val	Ala	Gly	Ser	Thr	
	445					450					455					460	
20	GGA	GCA	GGC	AAG	ACT	TCA	CTT	CTA	ATG	ATG	ATT	ATG	GGA	GAA	CTG	GAG	1560
	Gly	Ala	Gly	Lys	Thr	Ser	Leu	Leu	Met	Met	Ile	Met	Gly	Glu	Leu	Glu	
				465					470						475		
25	CCT	TCA	GAG	GGT	AAA	ATT	AAG	CAC	AGT	GGA	AGA	ATT	TCA	TTC	TGT	TCT	1608
	Pro	Ser	Glu	Gly	Lys	Ile	Lys	His	Ser	Gly	Arg	Ile	Ser	Phe	Cys	Ser	
				480				485						490			
30	CAG	TTT	TCC	TGG	ATT	ATG	CCT	GGC	ACC	ATT	AAA	GAA	AAT	ATC	ATC	TTT	1656
	Gln	Phe	Ser	Trp	Ile	Met	Pro	Gly	Thr	Ile	Lys	Glu	Asn	Ile	Ile	Phe	
			495					500					505				
35	GGT	GTT	TCC	TAT	GAT	GAA	TAT	AGA	TAC	AGA	AGC	GTC	ATC	AAA	GCA	TGC	1704
	Gly	Val	Ser	Tyr	Asp	Glu	Tyr	Arg	Tyr	Arg	Ser	Val	Ile	Lys	Ala	Cys	
		510					515					520					
40	CAA	CTA	GAA	GAG	GAC	ATC	TCC	AAG	TTT	GCA	GAG	AAA	GAC	AAT	ATA	GTT	1752
	Gln	Leu	Glu	Glu	Asp	Ile	Ser	Lys	Phe	Ala	Glu	Lys	Asp	Asn	Ile	Val	
	525					530					535					540	
45	CTT	GGA	GAA	GGT	GGA	ATC	ACA	CTG	AGT	GGA	GGT	CAA	CGA	GCA	AGA	ATT	1800
	Leu	Gly	Glu	Gly	Gly	Ile	Thr	Leu	Ser	Gly	Gly	Gln	Arg	Ala	Arg	Ile	
				545						550					555		
50	TCT	TTA	GCA	AGA	GCA	GTA	TAC	AAA	GAT	GCT	GAT	TTG	TAT	TTA	TTA	GAC	1848
	Ser	Leu	Ala	Arg	Ala	Val	Tyr	Lys	Asp	Ala	Asp	Leu	Tyr	Leu	Leu	Asp	
				560					565					570			
55	TCT	CCT	TTT	GGA	TAC	CTA	GAT	GTT	TTA	ACA	GAA	AAA	GAA	ATA	TTT	GAA	1896
	Ser	Pro	Phe	Gly	Tyr	Leu	Asp	Val	Leu	Thr	Glu	Lys	Glu	Ile	Phe	Glu	
			575					580					585				
60	AGC	TGT	GTC	TGT	AAA	CTG	ATG	GCT	AAC	AAA	ACT	AGG	ATT	TTG	GTC	ACT	1944
	Ser	Cys	Val	Cys	Lys	Leu	Met	Ala	Asn	Lys	Thr	Arg	Ile	Leu	Val	Thr	
		590					595					600					
65	TCT	AAA	ATG	GAA	CAT	TTA	AAG	AAA	GCT	GAC	AAA	ATA	TTA	ATT	TTG	CAT	1992
	Ser	Lys	Met	Glu	His	Leu	Lys	Lys	Ala	Asp	Lys	Ile	Leu	Ile	Leu	His	
	605					610					615					620	

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	GAA GGT AGC AGC TAT TTT TAT GGG ACA TTT TCA GAA CTC CAA AAT CTA	2040
	Glu Gly Ser Ser Tyr Phe Tyr Gly Thr Phe Ser Glu Leu Gln Asn Leu	
	625 630 635	
5	CAG CCA GAC TTT AGC TCA AAA CTC ATG GGA TGT GAT TCT TTC GAC CAA	2088
	Gln Pro Asp Phe Ser Ser Lys Leu Met Gly Cys Asp Ser Phe Asp Gln	
	640 645 650	
10	TTT AGT GCA GAA AGA AGA AAT TCA ATC CTA ACT GAG ACC TTA CAC CGT	2136
	Phe Ser Ala Glu Arg Arg Asn Ser Ile Leu Thr Glu Thr Leu His Arg	
	655 660 665	
15	TTC TCA TTA GAA GGA GAT GCT CCT GTC TCC TGG ACA GAA ACA AAA AAA	2184
	Phe Ser Leu Glu Gly Asp Ala Pro Val Ser Trp Thr Glu Thr Lys Lys	
	670 675 680	
20	CAA TCT TTT AAA CAG ACT GGA GAG TTT GGG GAA AAA AGG AAG AAT TCT	2232
	Gln Ser Phe Lys Gln Thr Gly Glu Phe Gly Glu Lys Arg Lys Asn Ser	
	685 690 695 700	
25	ATT CTC AAT CCA ATC AAC TCT ATA CGA AAA TTT TCC ATT GTG CAA AAG	2280
	Ile Leu Asn Pro Ile Asn Ser Ile Arg Lys Phe Ser Ile Val Gln Lys	
	705 710 715	
	ACT CCC TTA CAA ATG AAT GGC ATC GAA GAG GAT TCT GAT GAG CCT TTA	2328
	Thr Pro Leu Gln Met Asn Gly Ile Glu Glu Asp Ser Asp Glu Pro Leu	
	720 725 730	
30	GAG AGA AGG CTG TCC TTA GTA CCA GAT TCT GAG CAG GGA GAG GCG ATA	2376
	Glu Arg Arg Leu Ser Leu Val Pro Asp Ser Glu Gln Gly Glu Ala Ile	
	735 740 745	
35	CTG CCT CGC ATC AGC GTG ATC AGC ACT GGC CCC ACG CTT CAG GCA CGA	2424
	Leu Pro Arg Ile Ser Val Ile Ser Thr Gly Pro Thr Leu Gln Ala Arg	
	750 755 760	
40	AGG AGG CAG TCT GTC CTG AAC CTG ATG ACA CAC TCA GTT AAC CAA GGT	2472
	Arg Arg Gln Ser Val Leu Asn Leu Met Thr His Ser Val Asn Gln Gly	
	765 770 775 780	
45	CAG AAC ATT CAC CGA AAG ACA ACA GCA TCC ACA CGA AAA GTG TCA CTG	2520
	Gln Asn Ile His Arg Lys Thr Thr Ala Ser Thr Arg Lys Val Ser Leu	
	785 790 795	
	GCC CCT CAG GCA AAC TTG ACT GAA CTG GAT ATA TAT TCA AGA AGG TTA	2568
	Ala Pro Gln Ala Asn Leu Thr Glu Leu Asp Ile Tyr Ser Arg Arg Leu	
	800 805 810	
50	TCT CAA GAA ACT GGC TTG GAA ATA AGT GAA GAA ATT AAC GAA GAA GAC	2616
	Ser Gln Glu Thr Gly Leu Glu Ile Ser Glu Glu Ile Asn Glu Glu Asp	
	815 820 825	
55	TTA AAG GAG TGC CTT TTT GAT GAT ATG GAG AGC ATA CCA GCA GTG ACT	2664
	Leu Lys Glu Cys Leu Phe Asp Asp Met Glu Ser Ile Pro Ala Val Thr	
	830 835 840	

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5	ACA TGG AAC ACA TAC CTT CGA TAT ATT ACT GTC CAC AAG AGC TTA ATT	2712
	Thr Trp Asn Thr Tyr Leu Arg Tyr Ile Thr Val His Lys Ser Leu Ile	
	845 850 855 860	
	TTT GTG CTA ATT TGG TGC TTA GTA ATT TTT CTG GCA GAG GTG GCT GCT	2760
	Phe Val Leu Ile Trp Cys Leu Val Ile Phe Leu Ala Glu Val Ala Ala	
10	865 870 875	
	TCT TTG GTT GTG CTG TGG CTC CTT GGA AAC ACT CCT CTT CAA GAC AAA	2808
	Ser Leu Val Val Leu Trp Leu Leu Gly Asn Thr Pro Leu Gln Asp Lys	
	880 885 890	
	GGG AAT AGT ACT CAT AGT AGA AAT AAC AGC TAT GCA GTG ATT ATC ACC	2856
15	Gly Asn Ser Thr His Ser Arg Asn Asn Ser Tyr Ala Val Ile Ile Thr	
	895 900 905	
	AGC ACC AGT TCG TAT TAT GTG TTT TAC ATT TAC GTG GGA GTA GCC GAC	2904
	Ser Thr Ser Ser Tyr Tyr Val Phe Tyr Ile Tyr Val Gly Val Ala Asp	
	910 915 920	
20	ACT TTG CTT GCT ATG GGA TTC TTC AGA GGT CTA CCA CTG GTG CAT ACT	2952
	Thr Leu Leu Ala Met Gly Phe Phe Arg Gly Leu Pro Leu Val His Thr	
	925 930 935 940	
	CTA ATC ACA GTG TCG AAA ATT TTA CAC CAC AAA ATG TTA CAT TCT GTT	3000
	Leu Ile Thr Val Ser Lys Ile Leu His His Lys Met Leu His Ser Val	
25	945 950 955	
	CTT CAA GCA CCT ATG TCA ACC CTC AAC ACG TTG AAA GCA GGT GGG ATT	3048
	Leu Gln Ala Pro Met Ser Thr Leu Asn Thr Leu Lys Ala Gly Gly Ile	
	960 965 970	
	CTT AAT AGA TTC TCC AAA GAT ATA GCA ATT TTG GAT GAC CTT CTG CCT	3096
30	Leu Asn Arg Phe Ser Lys Asp Ile Ala Ile Leu Asp Asp Leu Leu Pro	
	975 980 985	
	CTT ACC ATA TTT GAC TTC ATC CAG TTG TTA TTA ATT GTG ATT GGA GCT	3144
	Leu Thr Ile Phe Asp Phe Ile Gln Leu Leu Leu Ile Val Ile Gly Ala	
	990 995 1000	
35	ATA GCA GTT GTC GCA GTT TTA CAA CCC TAC ATC TTT GTT GCA ACA GTG	3192
	Ile Ala Val Val Ala Val Leu Gln Pro Tyr Ile Phe Val Ala Thr Val	
	1005 1010 1015 1020	
	CCA GTG ATA GTG GCT TTT ATT ATG TTG AGA GCA TAT TTC CTC CAA ACC	3240
	Pro Val Ile Val Ala Phe Ile Met Leu Arg Ala Tyr Phe Leu Gln Thr	
40	1025 1030 1035	
	TCA CAG CAA CTC AAA CAA CTG GAA TCT GAA GGC AGG AGT CCA ATT TTC	3288
	Ser Gln Gln Leu Lys Gln Leu Glu Ser Glu Gly Arg Ser Pro Ile Phe	
	1040 1045 1050	
	ACT CAT CTT GTT ACA AGC TTA AAA GGA CTA TGG ACA CTT CGT GCC TTC	3336
45	Thr His Leu Val Thr Ser Leu Lys Gly Leu Trp Thr Leu Arg Ala Phe	
	1055 1060 1065	

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	GGA CGG CAG CCT TAC TTT GAA ACT CTG TTC CAC AAA GCT CTG AAT TTA	3384
	Gly Arg Gln Pro Tyr Phe Glu Thr Leu Phe His Lys Ala Leu Asn Leu	
	1070 1075 1080	
5	CAT ACT GCC AAC TGG TTC TTG TAC CTG TCA ACA CTG CGC TGG TTC CAA	3432
	His Thr Ala Asn Trp Phe Leu Tyr Leu Ser Thr Leu Arg Trp Phe Gln	
	1085 1090 1095 1100	
10	ATG AGA ATA GAA ATG ATT TTT GTC ATC TTC TTC ATT GCT GTT ACC TTC	3480
	Met Arg Ile Glu Met Ile Phe Val Ile Phe Phe Ile Ala Val Thr Phe	
	1105 1110 1115	
15	ATT TCC ATT TTA ACA ACA GGA GAA GGA GAA GGA AGA GTT GGT ATT ATC	3528
	Ile Ser Ile Leu Thr Thr Gly Glu Gly Glu Gly Arg Val Gly Ile Ile	
	1120 1125 1130	
20	CTG ACT TTA GCC ATG AAT ATC ATG AGT ACA TTG CAG TGG GCT GTA AAC	3576
	Leu Thr Leu Ala Met Asn Ile Met Ser Thr Leu Gln Trp Ala Val Asn	
	1135 1140 1145	
25	TCC AGC ATA GAT GTG GAT AGC TTG ATG CGA TCT GTG AGC CGA GTC TTT	3624
	Ser Ser Ile Asp Val Asp Ser Leu Met Arg Ser Val Ser Arg Val Phe	
	1150 1155 1160	
30	AAG TTC ATT GAC ATG CCA ACA GAA GGT AAA CCT ACC AAG TCA ACC AAA	3672
	Lys Phe Ile Asp Met Pro Thr Glu Gly Lys Pro Thr Lys Ser Thr Lys	
	1165 1170 1175 1180	
35	CCA TAC AAG AAT GGC CAA CTC TCG AAA GTT ATG ATT ATT GAG AAT TCA	3720
	Pro Tyr Lys Asn Gly Gln Leu Ser Lys Val Met Ile Ile Glu Asn Ser	
	1185 1190 1195	
40	CAC GTG AAG AAA GAT GAC ATC TGG CCC TCA GGG GGC CAA ATG ACT GTC	3768
	His Val Lys Lys Asp Asp Ile Trp Pro Ser Gly Gly Gln Met Thr Val	
	1200 1205 1210	
45	AAA GAT CTC ACA GCA AAA TAC ACA GAA GGT GGA AAT GCC ATA TTA GAG	3816
	Lys Asp Leu Thr Ala Lys Tyr Thr Glu Gly Gly Asn Ala Ile Leu Glu	
	1215 1220 1225	
50	AAC ATT TCC TTC TCA ATA AGT CCT GGC CAG AGG GTG GGC CTC TTG GGA	3864
	Asn Ile Ser Phe Ser Ile Ser Pro Gly Gln Arg Val Gly Leu Leu Gly	
	1230 1235 1240	
55	AGA ACT GGA TCA GGG AAG AGT ACT TTG TTA TCA GCT TTT TTG AGA CTA	3912
	Arg Thr Gly Ser Gly Lys Ser Thr Leu Leu Ser Ala Phe Leu Arg Leu	
	1245 1250 1255 1260	
60	CTG AAC ACT GAA GGA GAA ATC CAG ATC GAT GGT GTG TCT TGG GAT TCA	3960
	Leu Asn Thr Glu Gly Glu Ile Gln Ile Asp Gly Val Ser Trp Asp Ser	
	1265 1270 1275	
65	ATA ACT TTG CAA CAG TGG AGG AAA GCC TTT GGA GTG ATA CCA CAG AAA	4008
	Ile Thr Leu Gln Gln Trp Arg Lys Ala Phe Gly Val Ile Pro Gln Lys	
	1280 1285 1290	

	GTA TTT ATT TTT TCT GGA ACA TTT AGA AAA AAC TTG GAT CCC TAT GAA	4056
	Val Phe Ile Phe Ser Gly Thr Phe Arg Lys Asn Leu Asp Pro Tyr Glu	
	1295 1300 1305	
5	CAG TGG AGT GAT CAA GAA ATA TGG AAA GTT GCA GAT GAG GTT GGG CTC	4104
	Gln Trp Ser Asp Gln Glu Ile Trp Lys Val Ala Asp Glu Val Gly Leu	
	1310 1315 1320	
10	AGA TCT GTG ATA GAA CAG TTT CCT GGG AAG CTT GAC TTT GTC CTT GTG	4152
	Arg Ser Val Ile Glu Gln Phe Pro Gly Lys Leu Asp Phe Val Leu Val	
	1325 1330 1335 1340	
15	GAT GGG GGC TGT GTC CTA AGC CAT GGC CAC AAG CAG TTG ATG TGC TTG	4200
	Asp Gly Gly Cys Val Leu Ser His Gly His Lys Gln Leu Met Cys Leu	
	1345 1350 1355	
20	GCT AGA TCT GTT CTC AGT AAG GCG AAG ATC TTG CTG CTT GAT GAA CCC	4248
	Ala Arg Ser Val Leu Ser Lys Ala Lys Ile Leu Leu Leu Asp Glu Pro	
	1360 1365 1370	
25	AGT GCT CAT TTG GAT CCA GTA ACA TAC CAA ATA ATT AGA AGA ACT CTA	4296
	Ser Ala His Leu Asp Pro Val Thr Tyr Gln Ile Ile Arg Arg Thr Leu	
	1375 1380 1385	
30	AAA CAA GCA TTT GCT GAT TGC ACA GTA ATT CTC TGT GAA CAC AGG ATA	4344
	Lys Gln Ala Phe Ala Asp Cys Thr Val Ile Leu Cys Glu His Arg Ile	
	1390 1395 1400	
35	GAA GCA ATG CTG GAA TGC CAA CAA TTT TTG GTC ATA GAA GAG AAC AAA	4392
	Glu Ala Met Leu Glu Cys Gln Gln Phe Leu Val Ile Glu Glu Asn Lys	
	1405 1410 1415 1420	
40	GTG CGG CAG TAC GAT TCC ATC CAG AAA CTG CTG AAC GAG AGG AGC CTC	4440
	Val Arg Gln Tyr Asp Ser Ile Gln Lys Leu Leu Asn Glu Arg Ser Leu	
	1425 1430 1435	
45	TTC CGG CAA GCC ATC AGC CCC TCC GAC AGG GTG AAG CTC TTT CCC CAC	4488
	Phe Arg Gln Ala Ile Ser Pro Ser Asp Arg Val Lys Leu Phe Pro His	
	1440 1445 1450	
50	CGG AAC TCA AGC AAG TGC AAG TCT AAG CCC CAG ATT GCT GCT CTG AAA	4536
	Arg Asn Ser Ser Lys Cys Lys Ser Lys Pro Gln Ile Ala Ala Leu Lys	
	1455 1460 1465	
55	GAG GAG ACA GAA GAA GAG GTG CAA GAT ACA AGG CTT TAGAGAGCAG	4582
	Glu Glu Thr Glu Glu Glu Val Gln Asp Thr Arg Leu	
	1470 1475 1480	
60	CATAAATGTT GACATGGGAC ATTTGCTCAT GGAATTGGAG CTCGTGGGAC AGTCACCTCA	4642
	TGGAATTGGA GCTCGTGGAA CAGTTACCTC TGCCTCAGAA AACAAGGATG AATTAAGTTT	4702
	TTTTTTAAAA AAGAAACATT TGGTAAGGGG AATTGAGGAC ACTGATATGG GTCTTGATAA	4762
	ATGGCTTCCT GGCAATAGTC AAATTGTGTG AAAGGTACTT CAAATCCTTG AAGATTTACC	4822
	ACTTGTGTTT TGCAAGCCAG ATTTTCCTGA AAACCCTTGC CATGTGCTAG TAATTGAAAA	4882

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GGCAGCTCTA AATGTCAATC AGCCTAGTTG ATCAGCTTAT TGTCTAGTGA AACTCGTTAA 4942
 TTTGTAGTGT TGGAGAAGAA CTGAAATCAT ACTTCTTAGG GTTATGATTA AGTAATGATA 5002
 5 ACTGGAAACT TCAGCGGTTT ATATAAGCTT GTATTCCTTT TTCTCTCCTC TCCCCATGAT 5062
 GTTTAGAAAC ACAACTATAT TGTTTGCTAA GCATTCCAAC TATCTCATTT CCAAGCAAGT 5122
 10 ATTAGAATAC CACAGGAACC ACAAGACTGC ACATCAAAAT ATGCCCCATT CAACATCTAG 5182
 TGAGCAGTCA GGAAAGAGAA CTTCCAGATC CTGGAAATCA GGGTTAGTAT TGTCCAGGTC 5242
 TACCAAAAAT CTCAATATTT CAGATAATCA CAATACATCC CTTACCTGGG AAAGGGCTGT 5302
 15 TATAATCTTT CACAGGGGAC AGGATGGTTC CCTTGATGAA GAAGTTGATA TGCCTTTTCC 5362
 CAACTCCAGA AAGTGACAAG CTCACAGACC TTTGAACTAG AGTTTAGCTG GAAAAGTATG 5422
 TTAGTGCAAA TTGTCACAGG ACAGCCCTTC TTTCCACAGA AGCTCCAGGT AGAGGGTGTG 5482
 20 TAAGTAGATA GGCCATGGGC ACTGTGGGTA GACACACATG AAGTCCAAGC ATTTAGATGT 5542
 ATAGGTTGAT GGTGGTATGT TTTCAGGCTA GATGTATGTA CTTCATGCTG TCTACACTAA 5602
 25 GAGAGAATGA GAGACACACT GAAGAAGCAC CAATCATGAA TTAGTTTTAT ATGCTTCTGT 5662
 TTTATAATTT TGTGAAGCAA AATTTTTTCT CTAGGAAATA TTTATTTTAA TAATGTTTCA 5722
 AACATATATT ACAATGCTGT ATTTTAAAG AATGATTATG AATTACATTT GTATAAAATA 5782
 30 ATTTTTATAT TTGAAATATT GACTTTTTAT GGCAGTAGTA TTTTATGAA ATATTATGTT 5842
 AAAACTGGGA CAGGGGAGAA CCTAGGGTGA TATTAACCAG GGGCCATGAA TCACCTTTTG 5902
 35 GTCTGGAGGG AAGCCTTGGG GCTGATCGAG TTGTTGCCCA CAGCTGTATG ATTCCCAGCC 5962
 AGACACAGCC TCTTAGATGC AGTTCTGAAG AAGATGGTAC CACCAGTCTG ACTGTTTCCA 6022
 TCAAGGGTAC ACTGCCTTCT CAACTCCAAA CTGACTCTTA AGAAGACTGC ATTATATTTA 6082
 40 TTA CTGTAAG AAAATATCAC TTGTCAATAA AATCCATACA TTTGTGT 6129

(2) INFORMATION FOR SEQ ID NO:2:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1480 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

55

Met Gln Arg Ser Pro Leu Glu Lys Ala Ser Val Val Ser Lys Leu Phe
 1 5 10 15

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	Phe	Ser	Trp	Thr	Arg	Pro	Ile	Leu	Arg	Lys	Gly	Tyr	Arg	Gln	Arg	Leu	
				20					25					30			
5	Glu	Leu	Ser	Asp	Ile	Tyr	Gln	Ile	Pro	Ser	Val	Asp	Ser	Ala	Asp	Asn	
			35					40					45				
	Leu	Ser	Glu	Lys	Leu	Glu	Arg	Glu	Trp	Asp	Arg	Glu	Leu	Ala	Ser	Lys	
			50				55					60					
10	Lys	Asn	Pro	Lys	Leu	Ile	Asn	Ala	Leu	Arg	Arg	Cys	Phe	Phe	Trp	Arg	
		65				70					75					80	
	Phe	Met	Phe	Tyr	Gly	Ile	Phe	Leu	Tyr	Leu	Gly	Glu	Val	Thr	Lys	Ala	
15					85					90					95		
	Val	Gln	Pro	Leu	Leu	Leu	Gly	Arg	Ile	Ile	Ala	Ser	Tyr	Asp	Pro	Asp	
				100					105					110			
20	Asn	Lys	Glu	Glu	Arg	Ser	Ile	Ala	Ile	Tyr	Leu	Gly	Ile	Gly	Leu	Cys	
			115					120					125				
	Leu	Leu	Phe	Ile	Val	Arg	Thr	Leu	Leu	Leu	His	Pro	Ala	Ile	Phe	Gly	
25			130				135					140					
	Leu	His	His	Ile	Gly	Met	Gln	Met	Arg	Ile	Ala	Met	Phe	Ser	Leu	Ile	
						150					155					160	
	Tyr	Lys	Lys	Thr	Leu	Lys	Leu	Ser	Ser	Arg	Val	Leu	Asp	Lys	Ile	Ser	
30					165					170					175		
	Ile	Gly	Gln	Leu	Val	Ser	Leu	Leu	Ser	Asn	Asn	Leu	Asn	Lys	Phe	Asp	
				180					185					190			
35	Glu	Gly	Leu	Ala	Leu	Ala	His	Phe	Val	Trp	Ile	Ala	Pro	Leu	Gln	Val	
			195					200					205				
	Ala	Leu	Leu	Met	Gly	Leu	Ile	Trp	Glu	Leu	Leu	Gln	Ala	Ser	Ala	Phe	
			210				215					220					
40	Cys	Gly	Leu	Gly	Phe	Leu	Ile	Val	Leu	Ala	Leu	Phe	Gln	Ala	Gly	Leu	
			225			230					235					240	
	Gly	Arg	Met	Met	Met	Lys	Tyr	Arg	Asp	Gln	Arg	Ala	Gly	Lys	Ile	Ser	
45					245					250					255		
	Glu	Arg	Leu	Val	Ile	Thr	Ser	Glu	Met	Ile	Glu	Asn	Ile	Gln	Ser	Val	
				260					265					270			
50	Lys	Ala	Tyr	Cys	Trp	Glu	Glu	Ala	Met	Glu	Lys	Met	Ile	Glu	Asn	Leu	
			275					280					285				
	Arg	Gln	Thr	Glu	Leu	Lys	Leu	Thr	Arg	Lys	Ala	Ala	Tyr	Val	Arg	Tyr	
			290				295					300					
55	Phe	Asn	Ser	Ser	Ala	Phe	Phe	Phe	Ser	Gly	Phe	Phe	Val	Val	Phe	Leu	
						310					315					320	

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	Ser	Val	Leu	Pro	Tyr	Ala	Leu	Ile	Lys	Gly	Ile	Ile	Leu	Arg	Lys	Ile	
					325					330					335		
5	Phe	Thr	Thr	Ile	Ser	Phe	Cys	Ile	Val	Leu	Arg	Met	Ala	Val	Thr	Arg	
				340					345					350			
	Gln	Phe	Pro	Trp	Ala	Val	Gln	Thr	Trp	Tyr	Asp	Ser	Leu	Gly	Ala	Ile	
			355					360					365				
10	Asn	Lys	Ile	Gln	Asp	Phe	Leu	Gln	Lys	Gln	Glu	Tyr	Lys	Thr	Leu	Glu	
		370					375					380					
	Tyr	Asn	Leu	Thr	Thr	Thr	Glu	Val	Val	Met	Glu	Asn	Val	Thr	Ala	Phe	
15	385					390					395					400	
	Trp	Glu	Glu	Gly	Phe	Gly	Glu	Leu	Phe	Glu	Lys	Ala	Lys	Gln	Asn	Asn	
				405						410					415		
20	Asn	Asn	Arg	Lys	Thr	Ser	Asn	Gly	Asp	Asp	Ser	Leu	Phe	Phe	Ser	Asn	
				420					425					430			
	Phe	Ser	Leu	Leu	Gly	Thr	Pro	Val	Leu	Lys	Asp	Ile	Asn	Phe	Lys	Ile	
			435					440					445				
25	Glu	Arg	Gly	Gln	Leu	Leu	Ala	Val	Ala	Gly	Ser	Thr	Gly	Ala	Gly	Lys	
		450					455					460					
	Thr	Ser	Leu	Leu	Met	Met	Ile	Met	Gly	Glu	Leu	Glu	Pro	Ser	Glu	Gly	
30	465					470					475					480	
	Lys	Ile	Lys	His	Ser	Gly	Arg	Ile	Ser	Phe	Cys	Ser	Gln	Phe	Ser	Trp	
				485						490					495		
35	Ile	Met	Pro	Gly	Thr	Ile	Lys	Glu	Asn	Ile	Ile	Phe	Gly	Val	Ser	Tyr	
			500					505						510			
	Asp	Glu	Tyr	Arg	Tyr	Arg	Ser	Val	Ile	Lys	Ala	Cys	Gln	Leu	Glu	Glu	
		515						520					525				
40	Asp	Ile	Ser	Lys	Phe	Ala	Glu	Lys	Asp	Asn	Ile	Val	Leu	Gly	Glu	Gly	
		530					535					540					
	Gly	Ile	Thr	Leu	Ser	Gly	Gly	Gln	Arg	Ala	Arg	Ile	Ser	Leu	Ala	Arg	
45	545					550					555					560	
	Ala	Val	Tyr	Lys	Asp	Ala	Asp	Leu	Tyr	Leu	Leu	Asp	Ser	Pro	Phe	Gly	
				565					570						575		
50	Tyr	Leu	Asp	Val	Leu	Thr	Glu	Lys	Glu	Ile	Phe	Glu	Ser	Cys	Val	Cys	
			580						585					590			
	Lys	Leu	Met	Ala	Asn	Lys	Thr	Arg	Ile	Leu	Val	Thr	Ser	Lys	Met	Glu	
			595					600					605				
55	His	Leu	Lys	Lys	Ala	Asp	Lys	Ile	Leu	Ile	Leu	His	Glu	Gly	Ser	Ser	
		610					615					620					

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	Tyr	Phe	Tyr	Gly	Thr	Phe	Ser	Glu	Leu	Gln	Asn	Leu	Gln	Pro	Asp	Phe	625	630	635	640
5	Ser	Ser	Lys	Leu	Met	Gly	Cys	Asp	Ser	Phe	Asp	Gln	Phe	Ser	Ala	Glu	645	650	655	
	Arg	Arg	Asn	Ser	Ile	Leu	Thr	Glu	Thr	Leu	His	Arg	Phe	Ser	Leu	Glu	660	665	670	
10	Gly	Asp	Ala	Pro	Val	Ser	Trp	Thr	Glu	Thr	Lys	Lys	Gln	Ser	Phe	Lys	675	680	685	
15	Gln	Thr	Gly	Glu	Phe	Gly	Glu	Lys	Arg	Lys	Asn	Ser	Ile	Leu	Asn	Pro	690	695	700	
	Ile	Asn	Ser	Ile	Arg	Lys	Phe	Ser	Ile	Val	Gln	Lys	Thr	Pro	Leu	Gln	705	710	715	720
20	Met	Asn	Gly	Ile	Glu	Glu	Asp	Ser	Asp	Glu	Pro	Leu	Glu	Arg	Arg	Leu	725	730	735	
	Ser	Leu	Val	Pro	Asp	Ser	Glu	Gln	Gly	Glu	Ala	Ile	Leu	Pro	Arg	Ile	740	745	750	
25	Ser	Val	Ile	Ser	Thr	Gly	Pro	Thr	Leu	Gln	Ala	Arg	Arg	Arg	Gln	Ser	755	760	765	
30	Val	Leu	Asn	Leu	Met	Thr	His	Ser	Val	Asn	Gln	Gly	Gln	Asn	Ile	His	770	775	780	
	Arg	Lys	Thr	Thr	Ala	Ser	Thr	Arg	Lys	Val	Ser	Leu	Ala	Pro	Gln	Ala	785	790	795	800
35	Asn	Leu	Thr	Glu	Leu	Asp	Ile	Tyr	Ser	Arg	Arg	Leu	Ser	Gln	Glu	Thr	805	810	815	
	Gly	Leu	Glu	Ile	Ser	Glu	Glu	Ile	Asn	Glu	Glu	Asp	Leu	Lys	Glu	Cys	820	825	830	
40	Leu	Phe	Asp	Asp	Met	Glu	Ser	Ile	Pro	Ala	Val	Thr	Thr	Trp	Asn	Thr	835	840	845	
45	Tyr	Leu	Arg	Tyr	Ile	Thr	Val	His	Lys	Ser	Leu	Ile	Phe	Val	Leu	Ile	850	855	860	
	Trp	Cys	Leu	Val	Ile	Phe	Leu	Ala	Glu	Val	Ala	Ala	Ser	Leu	Val	Val	865	870	875	880
50	Leu	Trp	Leu	Leu	Gly	Asn	Thr	Pro	Leu	Gln	Asp	Lys	Gly	Asn	Ser	Thr	885	890	895	
	His	Ser	Arg	Asn	Asn	Ser	Tyr	Ala	Val	Ile	Ile	Thr	Ser	Thr	Ser	Ser	900	905	910	
55	Tyr	Tyr	Val	Phe	Tyr	Ile	Tyr	Val	Gly	Val	Ala	Asp	Thr	Leu	Leu	Ala	915	920	925	

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	Met Gly Phe Phe Arg Gly Leu Pro Leu Val His Thr Leu Ile Thr Val	
	930 935 940	
5	Ser Lys Ile Leu His His Lys Met Leu His Ser Val Leu Gln Ala Pro	
	945 950 955 960	
	Met Ser Thr Leu Asn Thr Leu Lys Ala Gly Gly Ile Leu Asn Arg Phe	
	965 970 975	
10	Ser Lys Asp Ile Ala Ile Leu Asp Asp Leu Leu Pro Leu Thr Ile Phe	
	980 985 990	
	Asp Phe Ile Gln Leu Leu Leu Ile Val Ile Gly Ala Ile Ala Val Val	
15	995 1000 1005	
	Ala Val Leu Gln Pro Tyr Ile Phe Val Ala Thr Val Pro Val Ile Val	
	1010 1015 1020	
20	Ala Phe Ile Met Leu Arg Ala Tyr Phe Leu Gln Thr Ser Gln Gln Leu	
	1025 1030 1035 1040	
	Lys Gln Leu Glu Ser Glu Gly Arg Ser Pro Ile Phe Thr His Leu Val	
	1045 1050 1055	
25	Thr Ser Leu Lys Gly Leu Trp Thr Leu Arg Ala Phe Gly Arg Gln Pro	
	1060 1065 1070	
	Tyr Phe Glu Thr Leu Phe His Lys Ala Leu Asn Leu His Thr Ala Asn	
30	1075 1080 1085	
	Trp Phe Leu Tyr Leu Ser Thr Leu Arg Trp Phe Gln Met Arg Ile Glu	
	1090 1095 1100	
35	Met Ile Phe Val Ile Phe Phe Ile Ala Val Thr Phe Ile Ser Ile Leu	
	1105 1110 1115 1120	
	Thr Thr Gly Glu Gly Glu Gly Arg Val Gly Ile Ile Leu Thr Leu Ala	
	1125 1130 1135	
40	Met Asn Ile Met Ser Thr Leu Gln Trp Ala Val Asn Ser Ser Ile Asp	
	1140 1145 1150	
	Val Asp Ser Leu Met Arg Ser Val Ser Arg Val Phe Lys Phe Ile Asp	
45	1155 1160 1165	
	Met Pro Thr Glu Gly Lys Pro Thr Lys Ser Thr Lys Pro Tyr Lys Asn	
	1170 1175 1180	
50	Gly Gln Leu Ser Lys Val Met Ile Ile Glu Asn Ser His Val Lys Lys	
	1185 1190 1195 1200	
	Asp Asp Ile Trp Pro Ser Gly Gly Gln Met Thr Val Lys Asp Leu Thr	
	1205 1210 1215	
55	Ala Lys Tyr Thr Glu Gly Gly Asn Ala Ile Leu Glu Asn Ile Ser Phe	
	1220 1225 1230	

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Ser Ile Ser Pro Gly Gln Arg Val Gly Leu Leu Gly Arg Thr Gly Ser
 1235 1240 1245
 5 Gly Lys Ser Thr Leu Leu Ser Ala Phe Leu Arg Leu Leu Asn Thr Glu
 1250 1255 1260
 Gly Glu Ile Gln Ile Asp Gly Val Ser Trp Asp Ser Ile Thr Leu Gln
 10 1265 1270 1275 1280
 Gln Trp Arg Lys Ala Phe Gly Val Ile Pro Gln Lys Val Phe Ile Phe
 1285 1290 1295
 Ser Gly Thr Phe Arg Lys Asn Leu Asp Pro Tyr Glu Gln Trp Ser Asp
 15 1300 1305 1310
 Gln Glu Ile Trp Lys Val Ala Asp Glu Val Gly Leu Arg Ser Val Ile
 1315 1320 1325
 Glu Gln Phe Pro Gly Lys Leu Asp Phe Val Leu Val Asp Gly Gly Cys
 20 1330 1335 1340
 Val Leu Ser His Gly His Lys Gln Leu Met Cys Leu Ala Arg Ser Val
 25 1345 1350 1355 1360
 Leu Ser Lys Ala Lys Ile Leu Leu Leu Asp Glu Pro Ser Ala His Leu
 1365 1370 1375
 Asp Pro Val Thr Tyr Gln Ile Ile Arg Arg Thr Leu Lys Gln Ala Phe
 30 1380 1385 1390
 Ala Asp Cys Thr Val Ile Leu Cys Glu His Arg Ile Glu Ala Met Leu
 1395 1400 1405
 Glu Cys Gln Gln Phe Leu Val Ile Glu Glu Asn Lys Val Arg Gln Tyr
 35 1410 1415 1420
 Asp Ser Ile Gln Lys Leu Leu Asn Glu Arg Ser Leu Phe Arg Gln Ala
 40 1425 1430 1435 1440
 Ile Ser Pro Ser Asp Arg Val Lys Leu Phe Pro His Arg Asn Ser Ser
 1445 1450 1455
 Lys Cys Lys Ser Lys Pro Gln Ile Ala Ala Leu Lys Glu Glu Thr Glu
 45 1460 1465 1470
 Glu Glu Val Gln Asp Thr Arg Leu
 1475 1480

50 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5635 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5	CATCATCAAT AATATACCTT ATTTTGGATT GAAGCCAATA TGATAATGAG GGGGTGGAGT	60
	TTGTGACGTG GCGCGGGGCG TGGGAACGGG GCGGGTGACG TAGTAGTGTG GCGGAAGTGT	120
	GATGTTGCAA GTGTGGCGGA ACACATGTAA GCGCCGGATG TGGTAAAAGT GACGTTTTTG	180
10	GTGTGCGCCG GTGTATACGG GAAGTGACAA TTTTCGCGCG GTTTTAGGCG GATGTTGTAG	240
	TAAATTTGGG CGTAACCAAG TAATGTTTGG CCATTTTCGC GGGAAACTG AATAAGAGGA	300
15	AGTGAAATCT GAATAATTCT GTGTTACTCA TAGCGCGTAA TATTTGTCTA GGGCCGCGGG	360
	GACTTTGACC GTTTACGTGG AGACTCGCCC AGGTGTTTTT CTCAGGTGTT TTCCGCGTTC	420
	CGGGTCAAAG TTGGCGTTTT ATTATTATAG TCAGCTGACG CGCAGTGTAT TTATACCCGG	480
20	TGAGTTCCTC AAGAGGCCAC TCTTGAGTGC CAGCGAGTAG AGTTTTCTCC TCCGAGCCGC	540
	TCCGAGCTAG TAACGGCCGC CAGTGTGCTG CAGATATCAA AGTCGACGGT ACCCGAGAGA	600
	CCATGCAGAG GTCGCCTCTG GAAAAGGCCA GCGTTGTCTC CAAACTTTTT TTCAGCTGGA	660
25	CCAGACCAAT TTTGAGGAAA GGATACAGAC AGCGCCTGGA ATTGTCAGAC ATATACCAA	720
	TCCCTTCTGT TGATTCTGCT GACAATCTAT CTGAAAAATT GGAAAGAGAA TGGGATAGAG	780
30	AGCTGGCTTC AAAGAAAAAT CCTAAACTCA TTAATGCCCT TCGGCGATGT TTTTCTGGA	840
	GATTTATGTT CTATGGAATC TTTTATATT TAGGGGAAGT CACCAAAGCA GTACAGCCTC	900
	TCTTACTGGG AAGAATCATA GCTTCCTATG ACCCGGATAA CAAGGAGGAA CGCTCTATCG	960
35	CGATTTATCT AGGCATAGGC TTATGCCTTC TCTTTATTGT GAGGACACTG CTCCTACACC	1020
	CAGCCATTTT TGGCCTTCAT CACATTGGAA TGCAGATGAG AATAGCTATG TTTAGTTTGA	1080
40	TTTATAAGAA GACTTTAAAG CTGTCAAGCC GTGTTCTAGA TAAAATAAGT ATTGGACAAC	1140
	TTGTTAGTCT CCTTTCCAAC AACCTGAACA AATTTGATGA AGGACTTGCA TTGGCACATT	1200
	TCGTGTGGAT CGCTCCTTTG CAAGTGGCAC TCCTCATGGG GCTAATCTGG GAGTTGTTAC	1260
45	AGGCGTCTGC CTTCTGTGGA CTTGGTTTCC TGATAGTCCT TGCCCTTTTT CAGGCTGGGC	1320
	TAGGGAGAAT GATGATGAAG TACAGAGATC AGAGAGCTGG GAAGATCAGT GAAAGACTTG	1380
50	TGATTACCTC AGAAATGATT GAAAACATCC AATCTGTTAA GGCATACTGC TGGGAAGAAG	1440
	CAATGGAAAA AATGATTGAA AACTTAAGAC AAACAGAACT GAAACTGACT CGGAAGGCAG	1500
	CCTATGTGAG ATACTTCAAT AGCTCAGCCT TCTTCTTCTC AGGGTTCTTT GTGGTGTTTT	1560
55	TATCTGTGCT TCCCTATGCA CTAATCAAAG GAATCATCCT CCGGAAAATA TTCACCACCA	1620
	TCTCATTCTG CATTGTTCTG CGCATGGCGG TCACTCGGCA ATTTCCCTGG GCTGTACAAA	1680

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	CATGGTATGA	CTCTCTTGGA	GCAATAAACA	AAATACAGGA	TTTCTTACAA	AAGCAAGAAT	1740
	ATAAGACATT	GGAATATAAC	TTAACGACTA	CAGAAGTAGT	GATGGAGAAT	GTAACAGCCT	1800
5	TCTGGGAGGA	GGGATTTGGG	GAATTATTTG	AGAAAGCAAA	ACAAAACAAT	AACAATAGAA	1860
	AAACTTCTAA	TGGTGATGAC	AGCCTCTTCT	TCAGTAATTT	CTCACTTCTT	GGTACTCCTG	1920
10	TCCTGAAAGA	TATTAATTTT	AAGATAGAAA	GAGGACAGTT	GTTGGCGGTT	GCTGGATCCA	1980
	CTGGAGCAGG	CAAGACTTCA	CTTCTAATGA	TGATTATGGG	AGAACTGGAG	CC' TTCAGAGG	2040
	GTAAAATTAA	GCACAGTGGA	AGAATTTTCAT	TCTGTTCTCA	GTTTTCCTGG	ATTATGCCTG	2100
15	GCACCATTAA	AGAAAATATC	ATCTTTGGTG	TTTCCTATGA	TGAATATAGA	TACAGAAGCG	2160
	TCATCAAAGC	ATGCCAACTA	GAAGAGGACA	TCTCCAAGTT	TGCAGAGAAA	GACAATATAG	2220
20	TTCTTGAGGA	AGGTGGAATC	ACACTGAGTG	GAGGTCAACG	AGCAAGAATT	TCTTTAGCAA	2280
	GAGCAGTATA	CAAAGATGCT	GATTTGTATT	TATTAGACTC	TCCTTTTGGA	TACCTAGATG	2340
	TTTTAACAGA	AAAAGAAATA	TTTGAAAGCT	GTGTCTGTAA	ACTGATGGCT	AACAAAAC TA	2400
25	GGATTTTGGT	CACTTCTAAA	ATGGAACATT	TAAAGAAAGC	TGACAAAATA	TTAATTTTGC	2460
	ATGAAGGTAG	CAGCTATTTT	TATGGGACAT	TTTCAGAACT	CCAAAATCTA	CAGCCAGACT	2520
30	TTAGCTCAAA	ACTCATGGGA	TGTGATTCTT	TCGACCAATT	TAGTGCAGAA	AGAAGAAATT	2580
	CAATCCTAAC	TGAGACCTTA	CACCGTTTCT	CATTAGAAGG	AGATGCTCCT	GTCTCCTGGA	2640
	CAGAAACAAA	AAAACAATCT	TTTAAACAGA	CTGGAGAGTT	TGGGGAAAAA	AGGAAGAATT	2700
35	CTATTCTCAA	TCCAATCAAC	TCTATACGAA	AATTTTCCAT	TGTGCAAAAG	ACTCCCTTAC	2760
	AAATGAATGG	CATCGAAGAG	GATTCTGATG	AGCCTTTAGA	GAGAAGGCTG	TCCTTAGTAC	2820
40	CAGATTCTGA	GCAGGGAGAG	GCGATACTGC	CTCGCATCAG	CGTGATCAGC	ACTGGCCCCA	2880
	CGCTTCAGGC	ACGAAGGAGG	CAGTCTGTCC	TGAACCTGAT	GACACACTCA	GTTAACCAAG	2940
	GTCAGAACAT	TCACCGAAAG	ACAACAGCAT	CCACACGAAA	AGTGTCACTG	GCCCCTCAGG	3000
45	CAAAC TTGAC	TGAAC TGGAT	ATATATTCAA	GAAGGTTATC	TCAAGAAACT	GGCTTGGA AA	3060
	TAAGTGAAGA	AATTAACGAA	GAAGACTTAA	AGGAGTGCCT	TTTTGATGAT	ATGGAGAGCA	3120
50	TACCAGCAGT	GACTACATGG	AACACATACC	TTGATATAT	TACTGTCCAC	AAGAGCTTAA	3180
	TTTTTGTGCT	AATTTGGTGC	TTAGTAATTT	TTCTGGCAGA	GGTGGCTGCT	TCTTTGGTTG	3240
	TGCTGTGGCT	CCTTGGA AAC	ACTCCTCTTC	AAGACAAAGG	GAATAGTACT	CATAGTAGAA	3300
55	ATAACAGCTA	TGCAGTGATT	ATCACCAGCA	CCAGTTCGTA	TTATGTGTTT	TACATTTACG	3360
	TGGGAGTAGC	CGACACTTTG	CTTGCTATGG	GATTCTTCAG	AGGTCTACCA	CTGGTGCATA	3420
	CTCTAATCAC	AGTGTCGAAA	ATTTTACACC	ACAAAATGTT	ACATTCTGTT	CTTCAAGCAC	3480

	CTATGTCAAC	CCTCAACACG	TTGAAAGCAG	GTGGGATTCT	TAATAGATTC	TCCAAAGATA	3540
5	TAGCAATTTT	GGATGACCTT	CTGCCTCTTA	CCATATTTGA	CTTCATCCAG	TTGTTATTAA	3600
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	TGCCAGTGAT	AGTGGCTTTT	ATTATGTTGA	GAGCATATTT	CCTCCAAACC	TCACAGCAAC	3720
10	TCAAACAAC	GGAATCTGAA	GGCAGGAGTC	CAATTTTCAC	TCATCTTGTT	ACAAGCTTAA	3780
	AAGGACTATG	GACACTTCGT	GCCTTCGGAC	GGCAGCCTTA	CTTTGAAACT	CTGTTCCACA	3840
15	AAGCTCTGAA	TTTACATACT	GCCAACGGT	TCTTGACCT	GTCAACACTG	CGCTGGTTCC	3900
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	TAACAACAGG	AGAAGGAGAA	GGAAGAGTTG	GTATTATCCT	GACTTTAGCC	ATGAATATCA	4020
20	TGAGTACATT	GCAGTGGGCT	GTAAACTCCA	GCATAGATGT	GGATAGCTTG	ATGCGATCTG	4080
	TGAGCCGAGT	CTTTAAGTTC	ATTGACATGC	CAACAGAAGG	TAAACCTACC	AAGTCAACCA	4140
25	AACCATACAA	GAATGGCCAA	CTCTCGAAAG	TTATGATTAT	TGAGAATTCA	CACGTGAAGA	4200
	AAGATGACAT	CTGGCCCTCA	GGGGGCCAAA	TGACTGTCAA	AGATCTCACA	GCAAAATACA	4260
	CAGAAGGTGG	AAATGCCATA	TTAGAGAACA	TTTCCTTCTC	AATAAGTCCT	GGCCAGAGGG	4320
30	TGGGCCTCTT	GGGAAGAACT	GGATCAGGGA	AGAGTACTTT	GTTATCAGCT	TTTTTGAGAC	4380
	TACTGAACAC	TGAAGGAGAA	ATCCAGATCG	ATGGTGTGTC	TTGGGATTCA	ATAACTTTGC	4440
35	AACAGTGGAG	GAAAGCCTTT	GGAGTGATAC	CACAGAAAGT	ATTTATTTTT	TCTGGAACAT	4500
	TTAGAAAAAA	CTTGGATCCC	TATGAACAGT	GGAGTGATCA	AGAAATATGG	AAAGTTGCAG	4560
	ATGAGGTTGG	GCTCAGATCT	GTGATAGAAC	AGTTTCCTGG	GAAGCTTGAC	TTTGTCTTGG	4620
40	TGGATGGGGG	CTGTGTCCTA	AGCCATGGCC	ACAAGCAGTT	GATGTGCTTG	GCTAGATCTG	4680
	TTCTCAGTAA	GGCGAAGATC	TTGCTGCTTG	ATGAACCCAG	TGCTCATTTG	GATCCAGTAA	4740
45	CATACCAAAT	AATTAGAAGA	ACTCTAAAAC	AAGCATTTGC	TGATTGCACA	GTAATTCTCT	4800
	GTGAACACAG	GATAGAAGCA	ATGCTGGAAT	GCCAACAATT	TTTGGTCATA	GAAGAGAACA	4860
	AAGTGCGGCA	GTACGATTCC	ATCCAGAAAC	TGCTGAACGA	GAGGAGCCTC	TTCCGGCAAG	4920
50	CCATCAGCCC	CTCCGACAGG	GTGAAGCTCT	TTCCCCACCG	GAAGTCAAGC	AAGTGCAAGT	4980
	CTAAGCCCCA	GATTGCTGCT	CTGAAAGAGG	AGACAGAAGA	AGAGGTGCAA	GATACAAGGC	5040
55	TTTAGAGAGC	AGCATAAATG	TTGACATGGG	ACATTTGCTC	ATGGAATTGG	AGGTAGCGGA	5100
	TTGAGGTACT	GAAATGTGTG	GGCGTGGCTT	AAGGGTGGGA	AAGAATATAT	AAGGTGGGGG	5160
	TCTCATGTAG	TTTTGTATCT	GTTTTGCAGC	AGCCGCCGCC	ATGAGCGCCA	ACTCGTTTGA	5220

- 113 -

TGGAAGCATT GTGAGCTCAT ATTTGACAAC GCGCATGCCC CCATGGGCCG GGGTGCCTCA 5280
GAATGTGATG GGCTCCAGCA TTGATGGTCG CCCCCTCCTG CCCGCAAACCT CTACTACCTT 5340
5 GACCTACGAG ACCGTGTCTG GAACGCCGTT GGAGACTGCA GCCTCCGCCG CCGCTTCAGC 5400
CGCTGCAGCC ACCGCCCCGCG GGATTGTGAC TGACTTTGCT TTCCTGAGCC CGCTTGCAAG 5460
CAGTGCAGCT TCCCGTTCAT CCGCCCGCGA TGACAAGTTG ACGGCTCTTT TGGCACAATT 5520
10 GGATTCTTTG ACCCGGGAAC TTAATGTCGT TTCTCAGCAG CTGTTGGATC TGCGCCAGCA 5580
GGTTTCTGCC CTGAAGGCTT CCTCCCCTCC CAATGCGGTT TAAAACATAA ATAAA 5635

15 (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

30 ACTCTTGAGT GCCAGCGAGT AGAGTTTTCT CCTCCG 36

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

45 GCAAAGGAGC GATCCACACG AAATGTGCC 29

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
50 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

- 114 -

CTCCTCCGAG CCGCTCCGAG CTAG

24

(2) INFORMATION FOR SEQ ID NO:7:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: cDNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCAAAAATGG CTGGGTGTAG GAGCAGTGTC C

31

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGATCCTTT ATTATAGGGG AAGTCCACGC CTAC

34

35

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: cDNA

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGGATCCAT CGATGAAATA TGACTACGTC CG

32

50

Claims

1. An adenovirus-based gene therapy vector comprising the genome of an adenovirus 2 serotype in which the Ela and Elb regions of the genome, which are involved in early stages of viral replication, have been deleted and replaced by genetic material of interest.
2. The adenovirus-based gene therapy vector of claim 1, wherein the genetic material of interest is DNA encoding cystic fibrosis transmembrane conductance regulator
3. The adenovirus-based gene therapy vector of claim 1 further comprising PGK promoter operably linked to the genetic material of interest.
4. The adenovirus-based gene therapy vector of claim 2 having substantially the same nucleotide sequence as shown in Table II (SEQ ID NO:3).
5. An adenovirus-based gene therapy vector comprising adenovirus inverted terminal repeat nucleotide sequences and the minimal nucleotide sequences necessary for efficient replication and packaging and genetic material of interest.
6. The adenovirus-based gene therapy vector of claim 5 having the adenovirus 2 sequences shown in Figure 17.
7. The adenovirus-based gene therapy vector of claim 5 further comprising PGK promoter operably linked to the genetic material of interest.
8. The adenovirus-based gene therapy vector of claim 5 in which the genetic material of interest is selected from the group consisting of DNA encoding: cystic fibrosis transmembrane conductance regulator, Factor VIII, and Factor IX.
9. An adenovirus-based gene therapy vector comprising an adenovirus genome which has been deleted for all E4 open reading frames, except open reading frame 6, and additionally comprising genetic material of interest.
10. The adenovirus-based gene therapy vector of claim 9 further comprising PGK promoter operably linked to the genetic material of interest.
11. The adenovirus-based gene therapy vector of claim 9 in which the Ela and Elb regions of the genome, which are involved in early stages of viral replication, have been deleted.

12. The adenovirus-based gene therapy vector of claim 9 in which the E3 region has been deleted.
13. An adenovirus-based gene therapy vector comprising an adenovirus genome which
5 has been deleted for all E4 open reading frames, except open reading frame 3, and additionally comprising genetic material of interest.
14. The adenovirus-based gene therapy vector of claim 13 in which the Ela and Elb
10 regions of the genome, which are involved in early stages of viral replication, have been deleted.
15. The adenovirus-based gene therapy vector of claim 13 further comprising PGK promoter operably linked to the genetic material of interest.
- 15 16. The adenovirus-based gene therapy vector of claim 13 in which the E3 region has been deleted.
17. A method for treating or preventing cystic fibrosis in a patient comprising
administering to the pulmonary airways of the patient, a gene therapy vector comprising
20 DNA encoding cystic fibrosis transmembrane conductance regulator.
18. The method of claim 17 wherein the gene therapy vector is an adenovirus-based gene therapy vector comprising the genome of an adenovirus 2 serotype in which the Ela and Elb
25 regions of the genome, which are involved in early stages of viral replication, have been deleted and replaced by DNA encoding cystic fibrosis transmembrane conductance regulator.
19. The method of claim 17 wherein the gene therapy vector further comprises PGK promoter operably linked to the DNA encoding cystic fibrosis transmembrane conductance
30 regulator.
20. The method of claim 17 wherein the gene therapy vector is an adenovirus-based gene therapy vector comprising adenovirus inverted terminal repeats and the minimal sequences necessary for efficient replication and packaging and DNA encoding cystic fibrosis
35 transmembrane conductance regulator.
21. The method of claim 20 wherein the gene therapy vector further comprises PGK promoter operably linked to the DNA encoding cystic fibrosis transmembrane conductance regulator.

22. The method of claim 17 wherein the gene therapy vector is an adenovirus-based gene therapy vector comprising an adenovirus genome which has been deleted for all E4 open reading frames, except open reading frame 6, and additionally comprising DNA encoding cystic fibrosis transmembrane conductance regulator.

23. The method of claim 22 wherein the gene therapy vector further comprises PGK promoter operably linked to the DNA encoding cystic fibrosis transmembrane conductance regulator.

24. The method of claim 17 wherein the gene therapy vector is an adenovirus-based gene therapy vector comprising an adenovirus genome which has been deleted for all E4 open reading frames, except open reading frame 6, and has been deleted for the Ela and Elb regions of the genome, which are involved in early stages of viral replication, and additionally comprising DNA encoding cystic fibrosis transmembrane conductance regulator.

25. The method of claim 24 wherein the gene therapy vector further comprises PGK promoter operably linked to the DNA encoding cystic fibrosis transmembrane conductance regulator.

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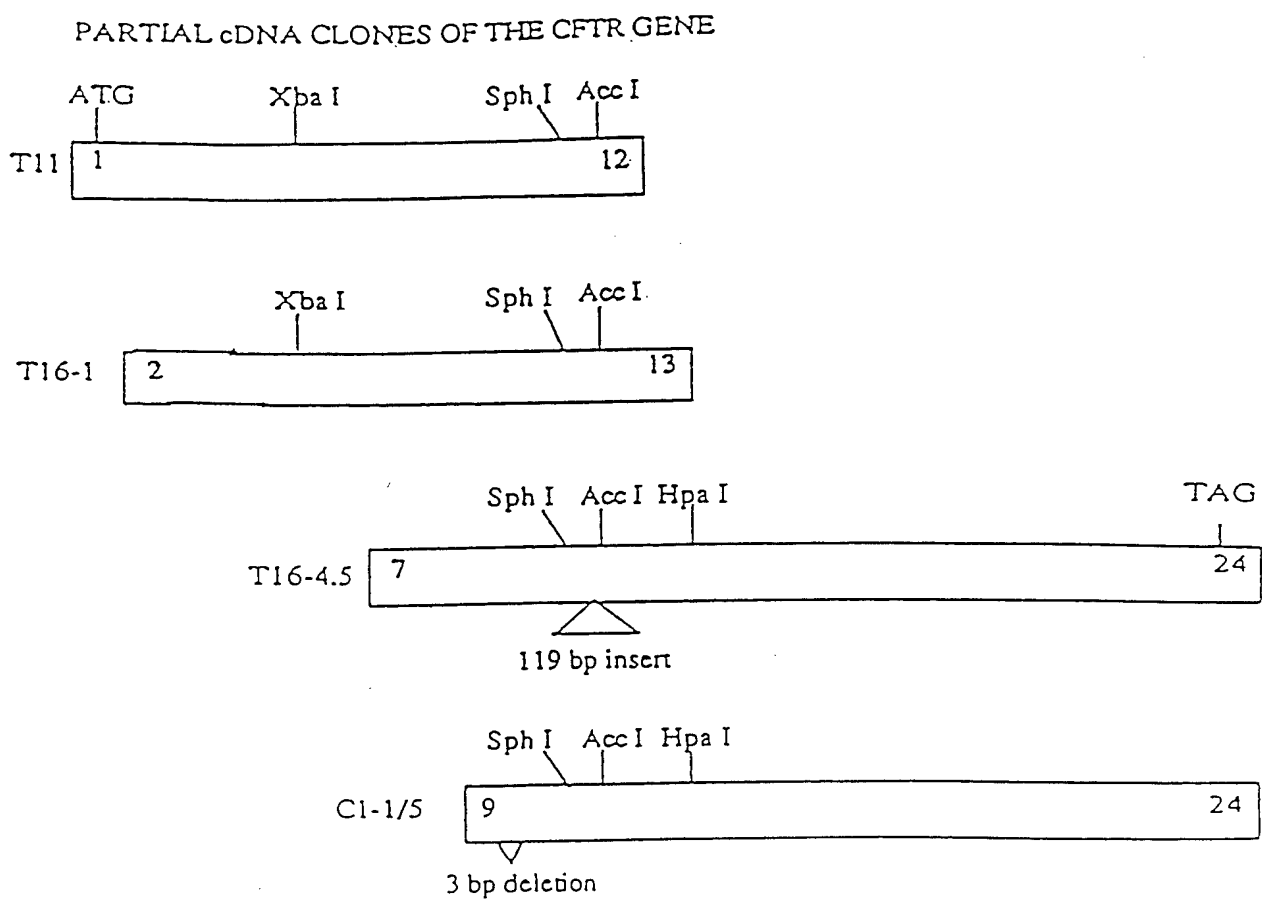


Figure 1

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STRATEGY FOR CONSTRUCTING pKK- CFTR1

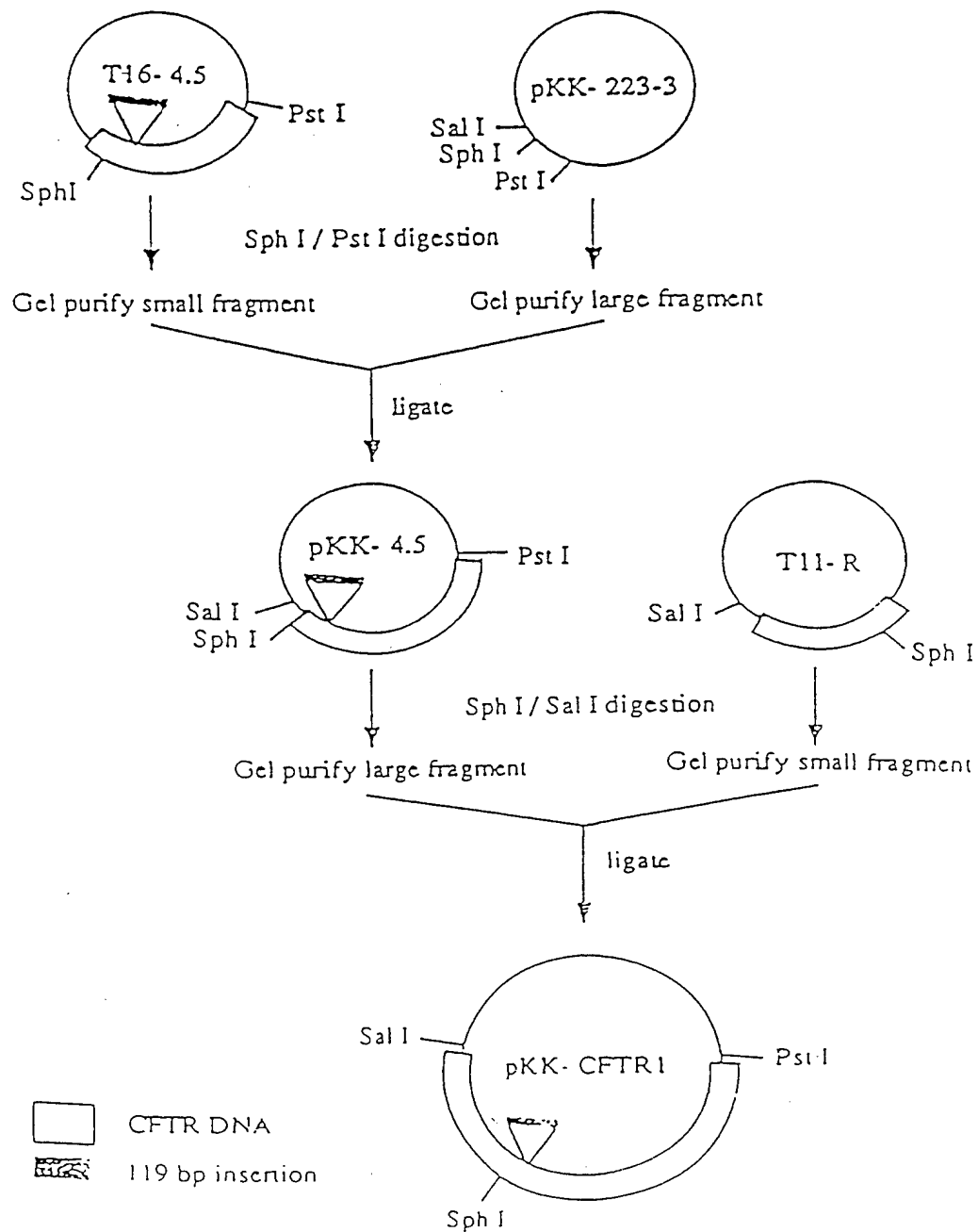


Figure 2

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CONSTRUCTION OF THE pKK- CFTR2 PLASMID

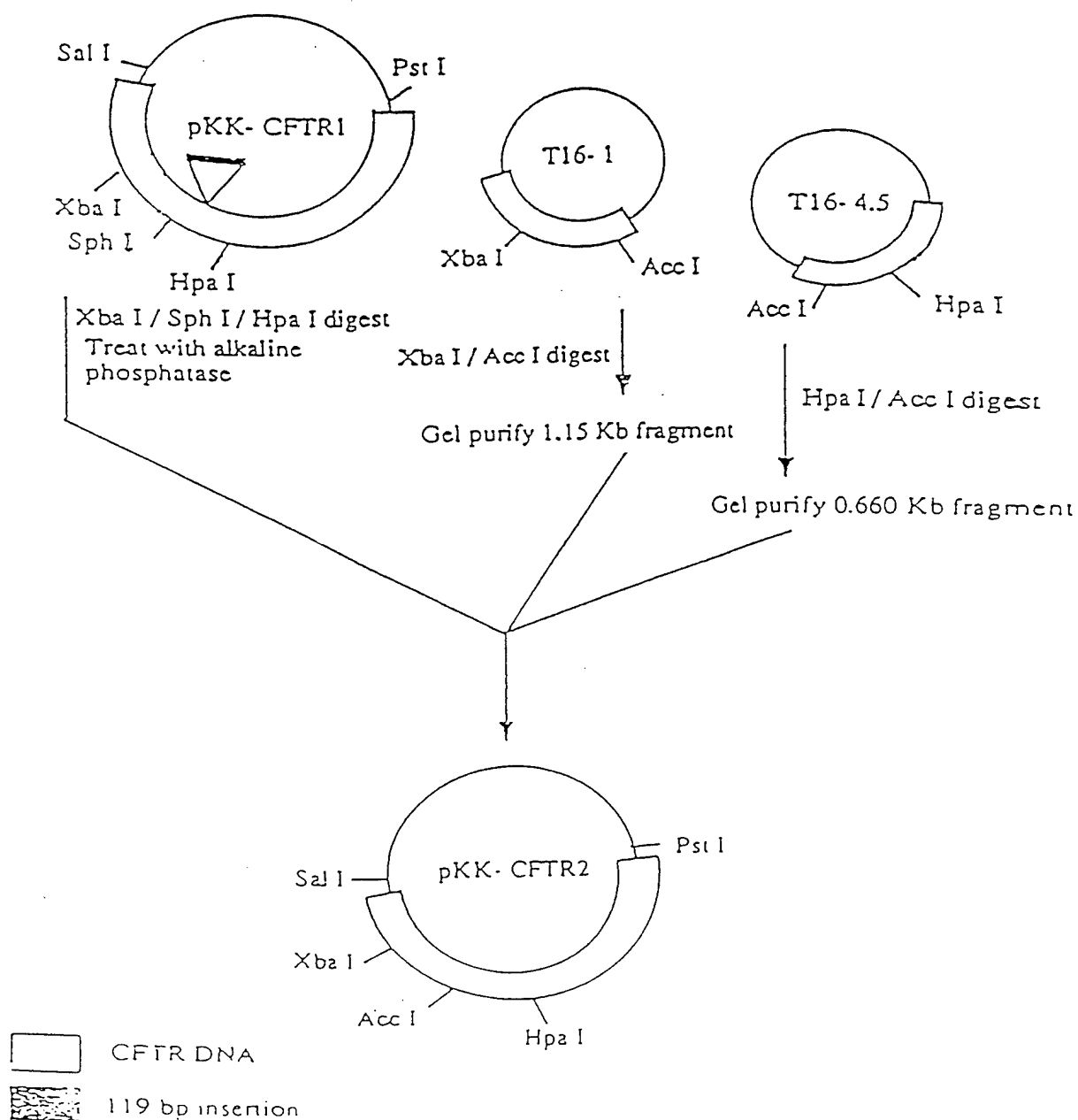


Figure 3

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STRATEGY FOR CONSTRUCTING THE pSC- CFTR2 PLASMID

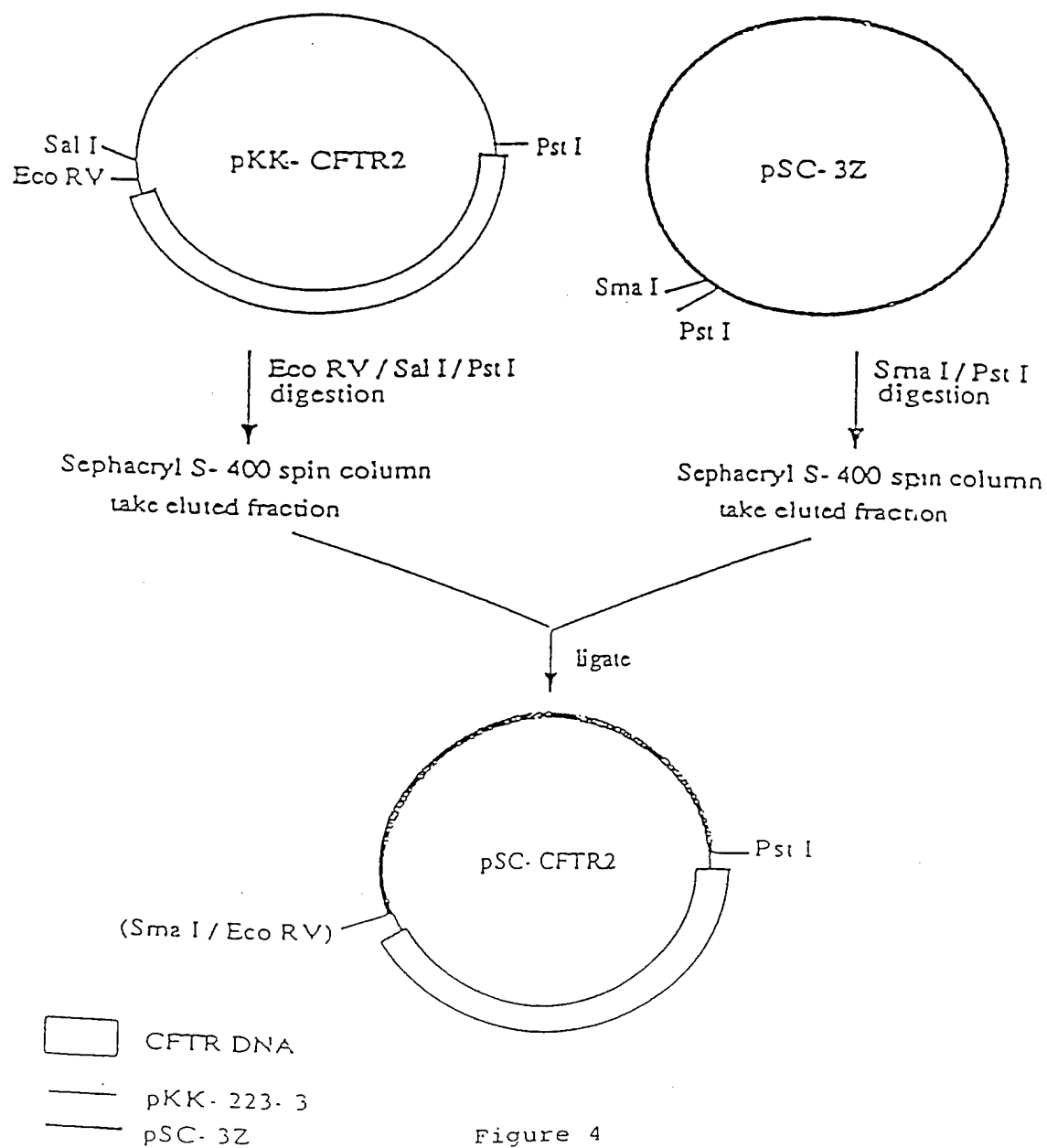


Figure 4

5/50

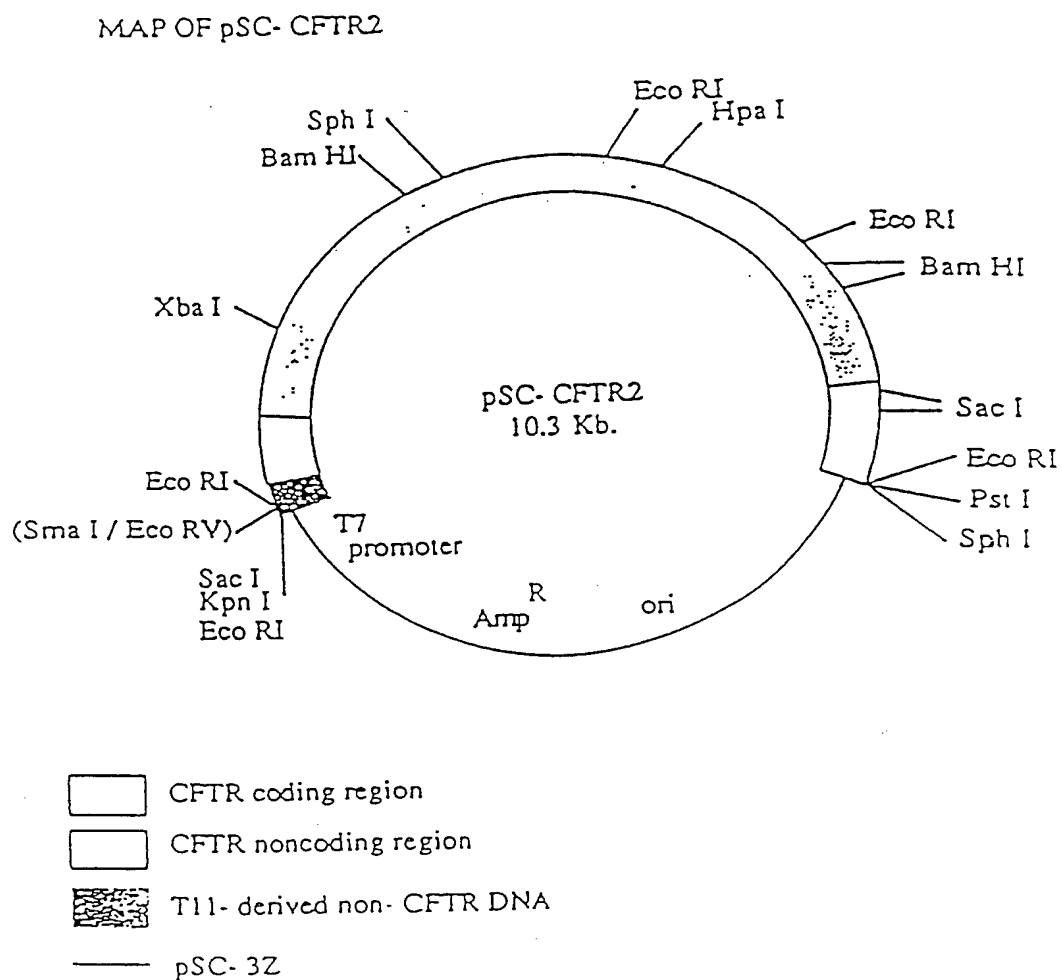


Figure 5

6/50

```

S          bp 1716
P          |
h          |<=====>Synthetic Intron=====>
I          |
|-----1195RG-----
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GTACGGTTGATCTTCTCCATTCCCCGAGTGGTCAAGTTTTAGACTTCACCTCTGTCCTG
<-----1198RG-----
                                     bp 1717
=====|
                                     |
----->|-----
CTGAGGTGACAATGACATCTACTCTGACATTCTCTCCTCAGGACATCTCCAAGTTTGCAG
GACTCCACTGTTACTGTAGATGAGACTGTAAGAGAGGAGTCCTGTAGAGGTTCAAACGTC
-----|<-----1197RG-----
                                     H
                                     i
                                     n
                                     c
                                     I
                                     I
-----1196RG----->
AGAAAGACAATATAGTTCTTGGAGAAGGTGGAATCACACTGAGTGGAGGTC
TCTTTCTGTTATATCAAGAACCTCTTCCACCTTAGTGTGACTCACCTCCAG
-----|

```

Figure 6

7/50

CONSTRUCTION OF THE pKK- CFTR3 cDNA

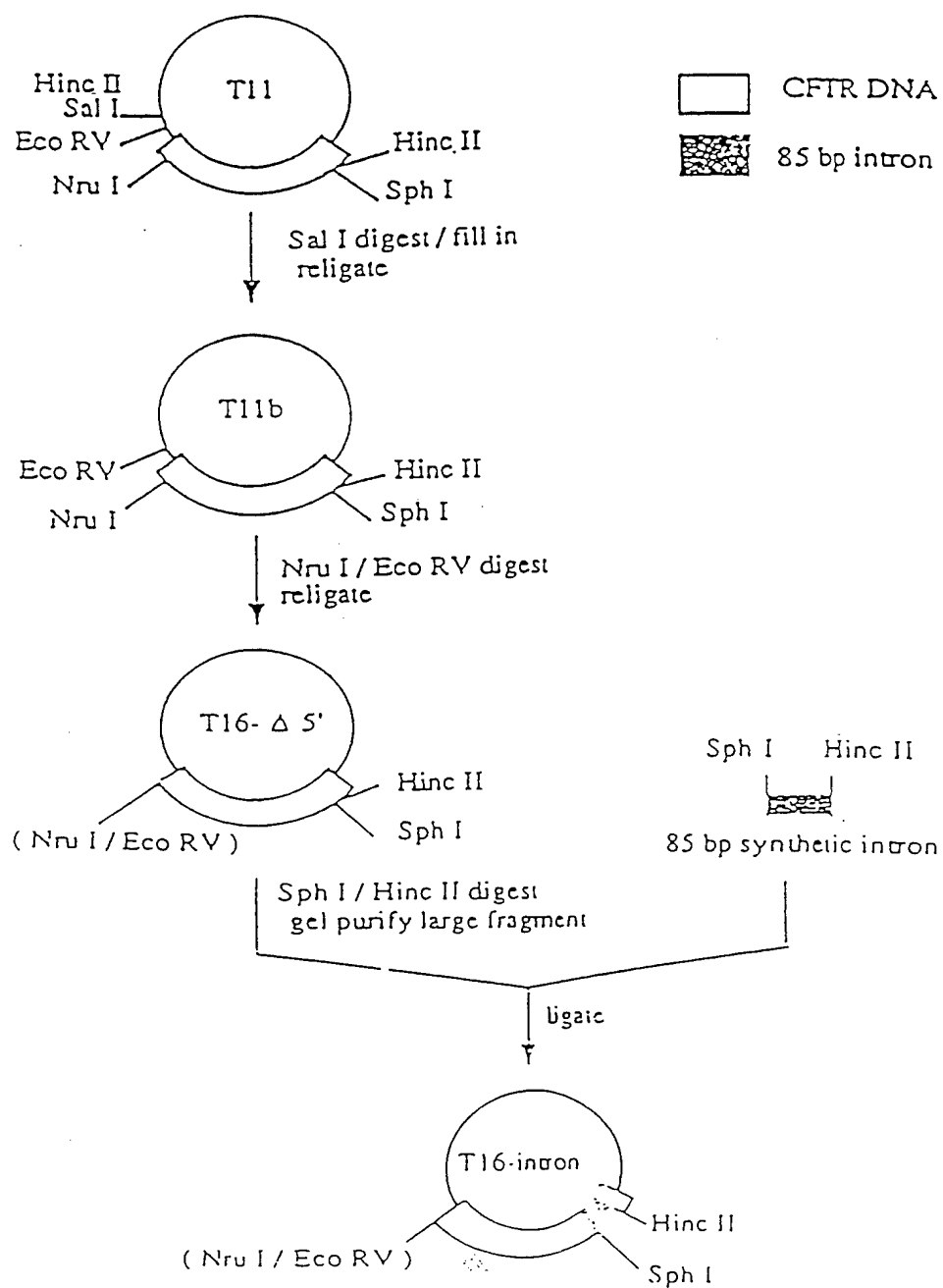


Figure 7A

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CONSTRUCTION OF THE pKK-CFTR3 CLONE (cont'd.)

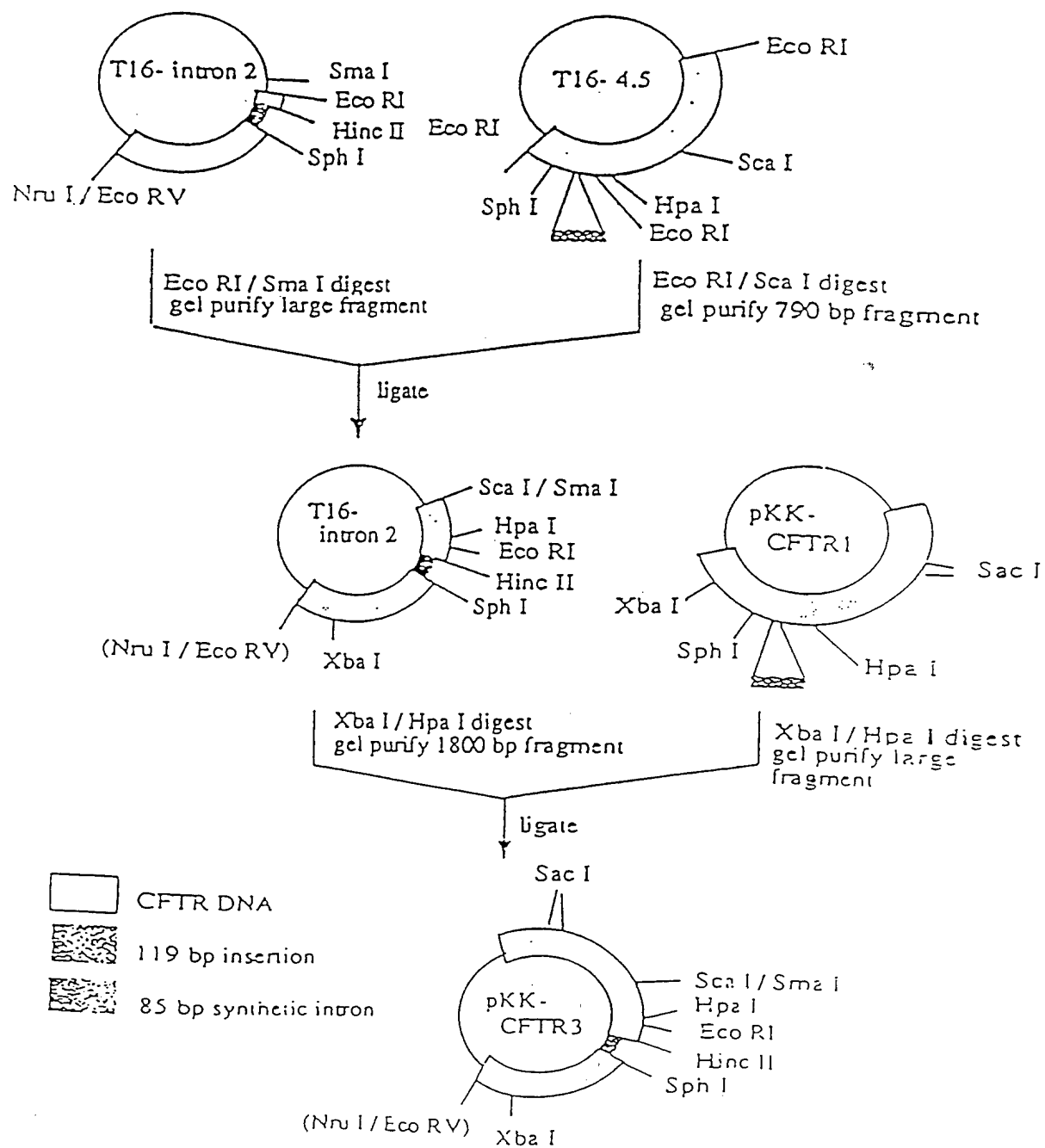
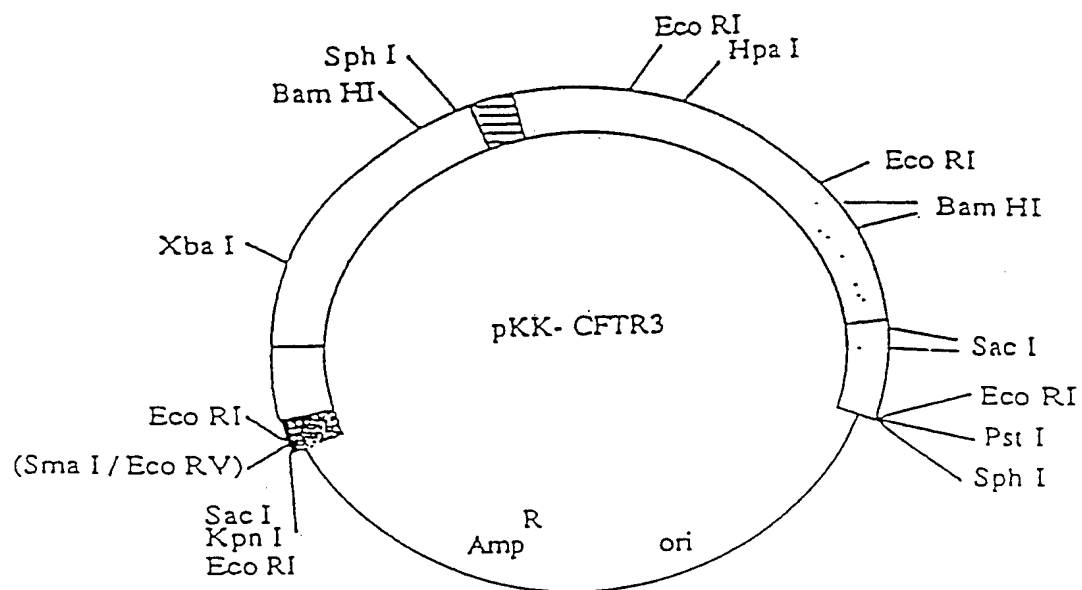


Figure 7B

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MAP OF pKK- CFTR3








-  CFTR coding region
-  CFTR noncoding region
-  85 bp intron
-  T11-derived non-CFTR DNA
-  pKK- 223- 3

Figure 8

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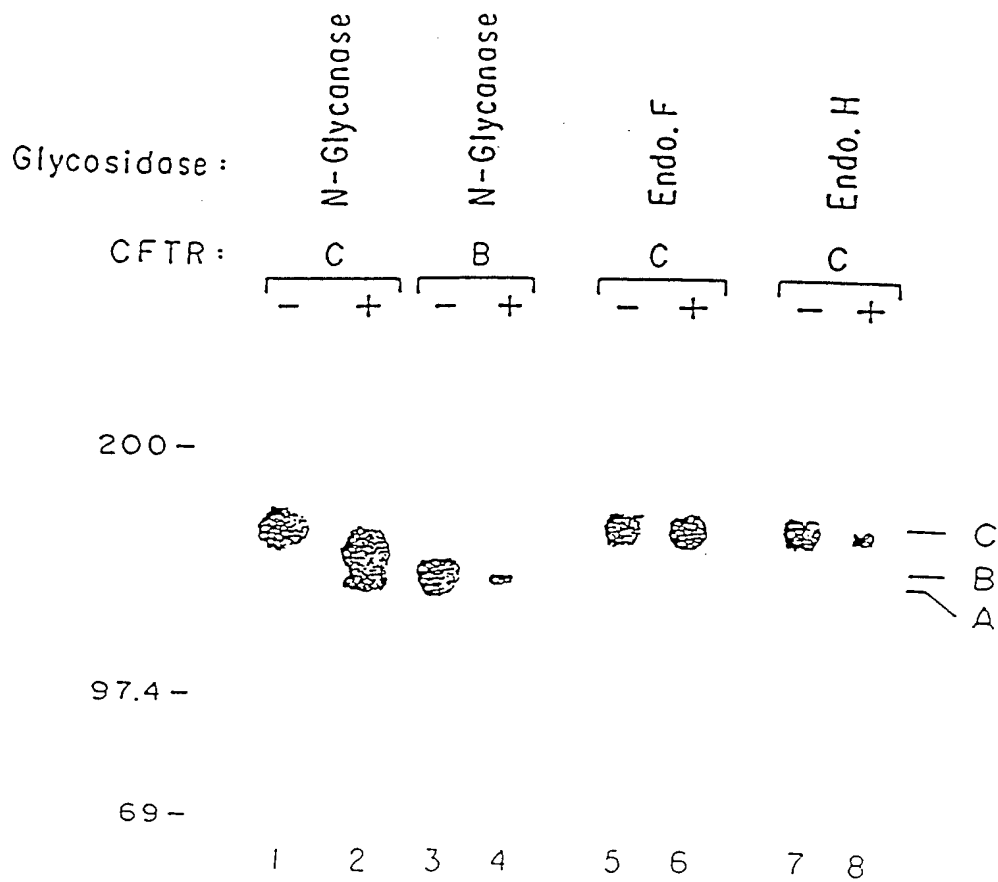


Figure 9

11/50

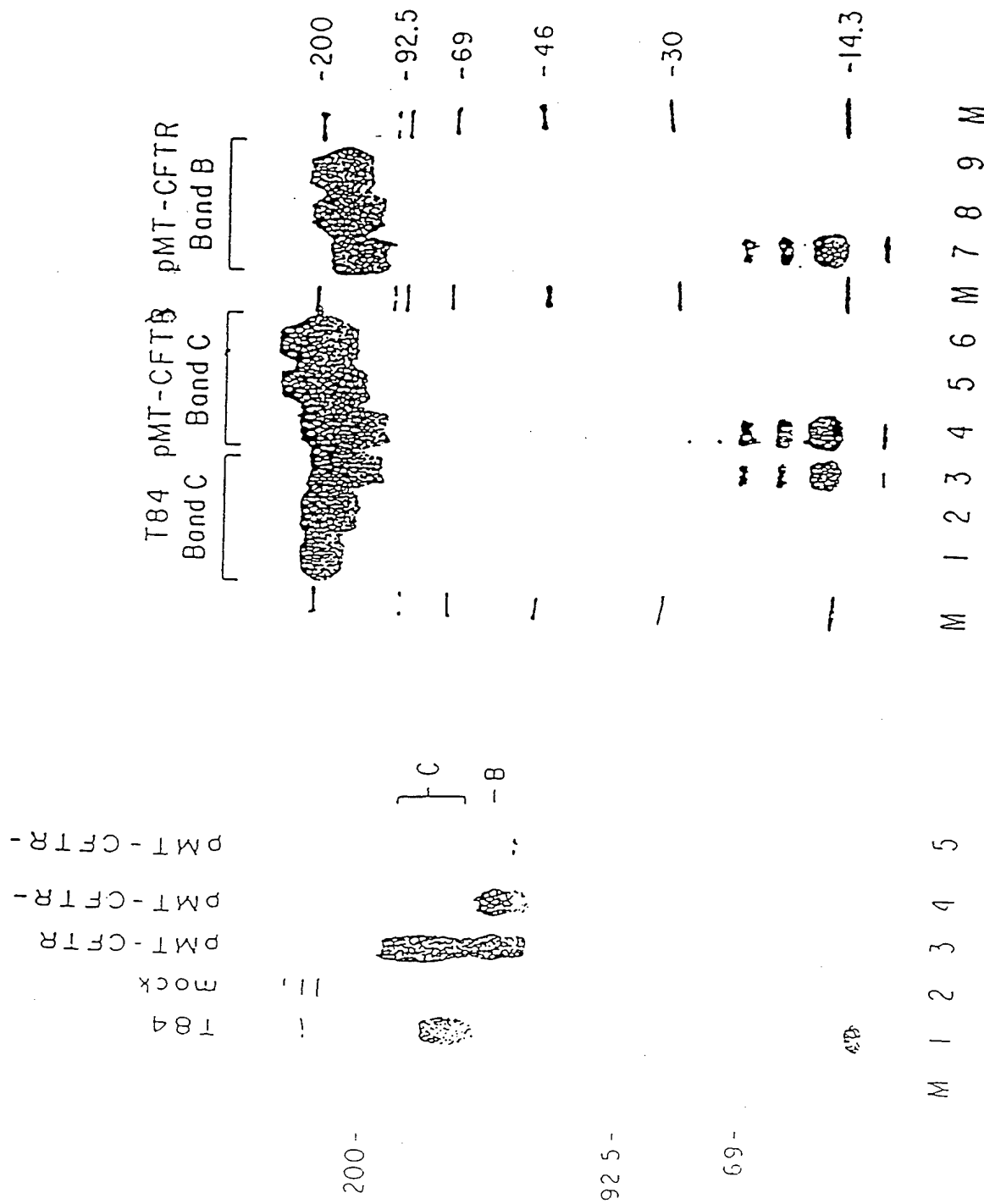


Figure 10B

Figure 10A

12/50

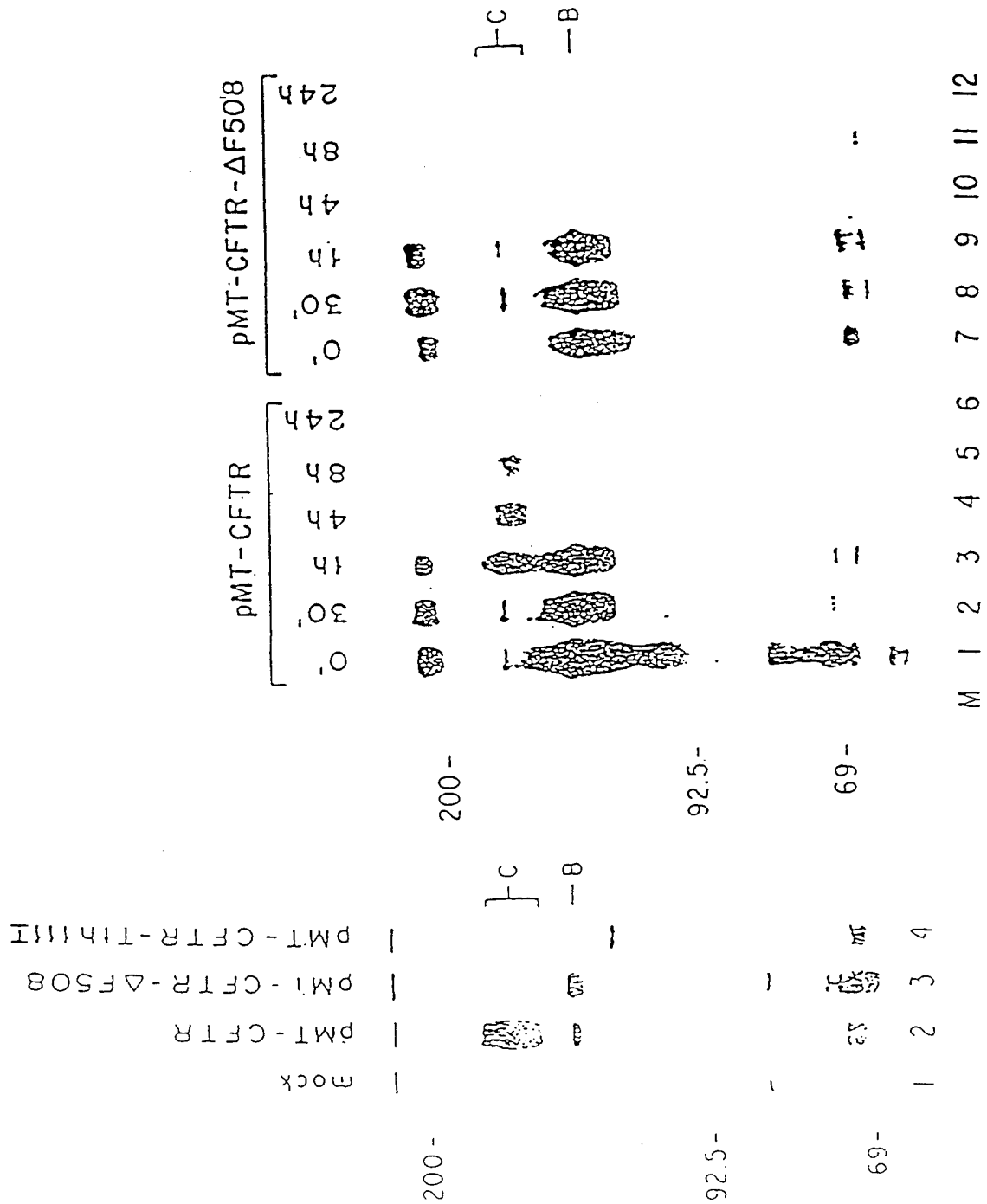


Figure 11A

Figure 11B

13/50

Figure 12A

Figure 12B

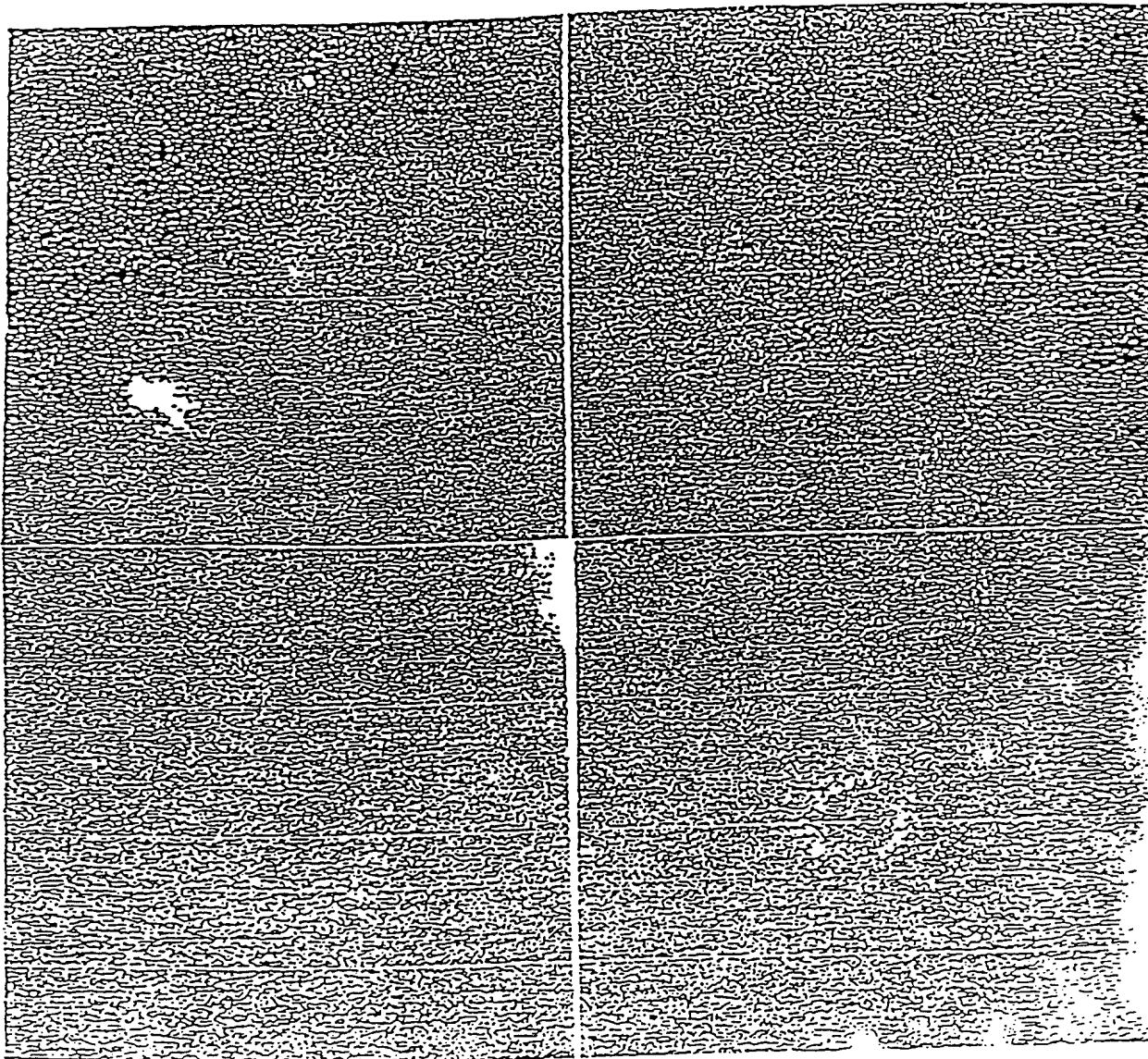


Figure 12C

Figure 12D

14/50

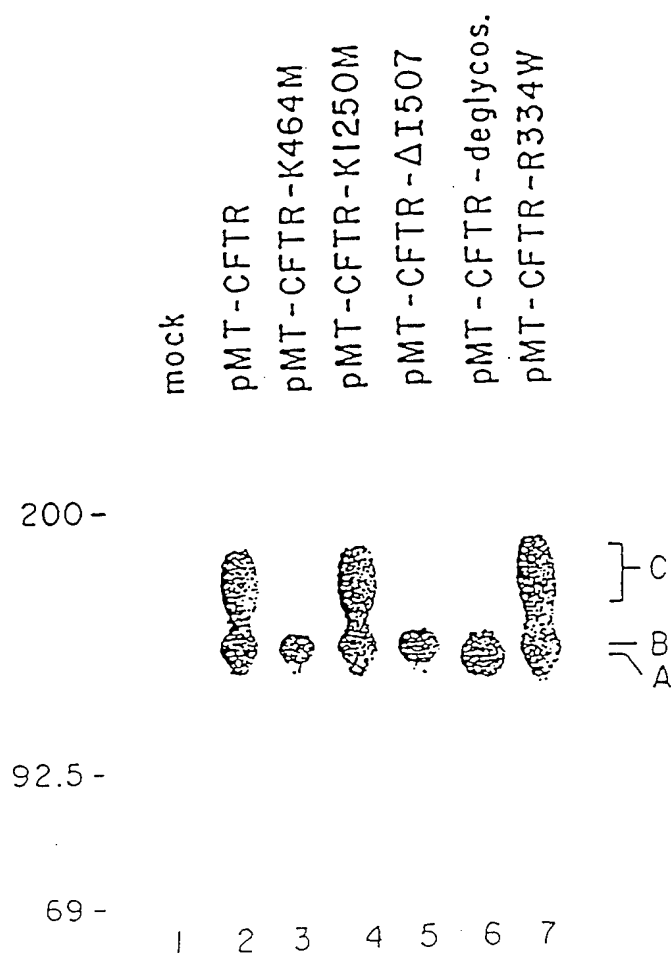


Figure 13

15/50

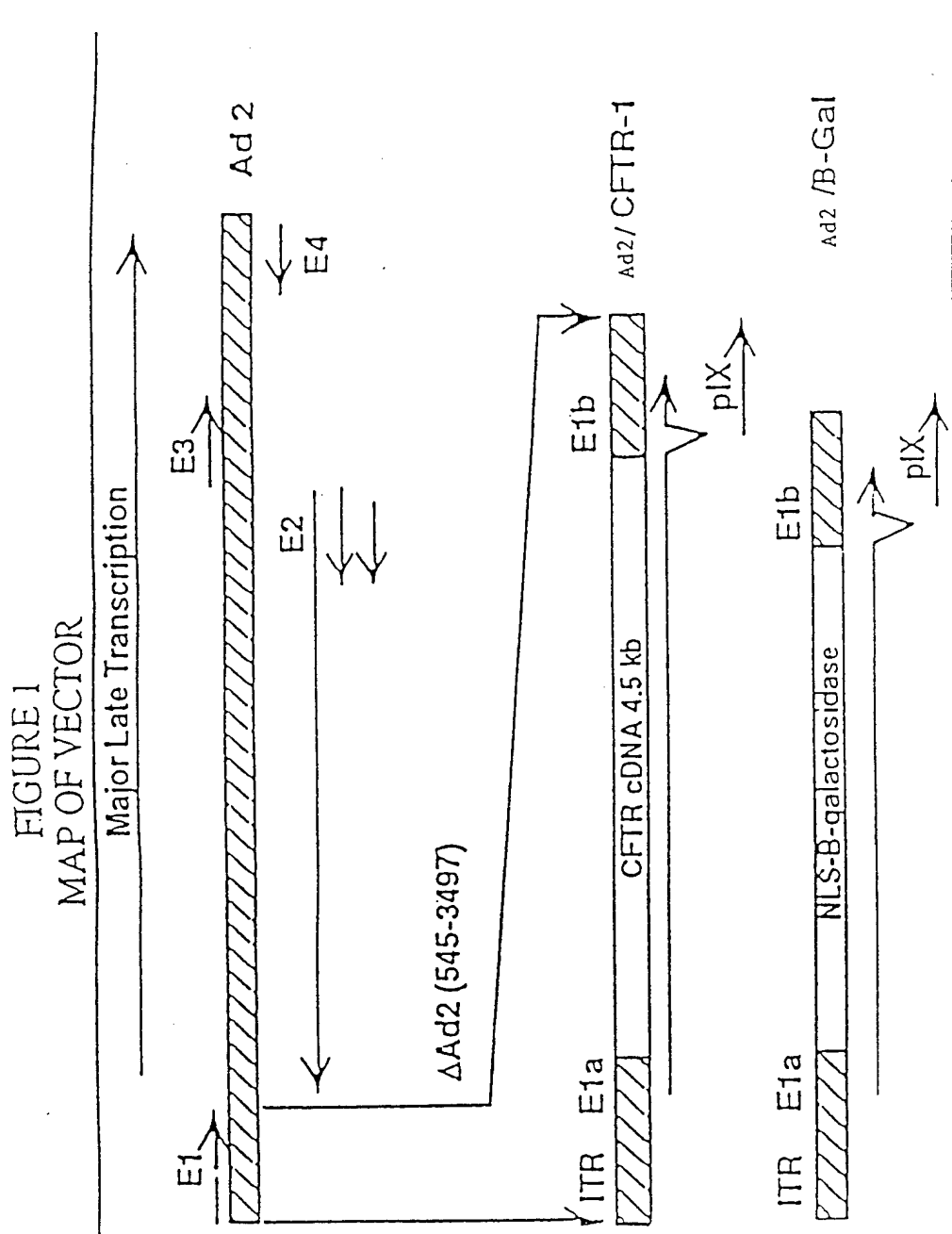


Figure 14

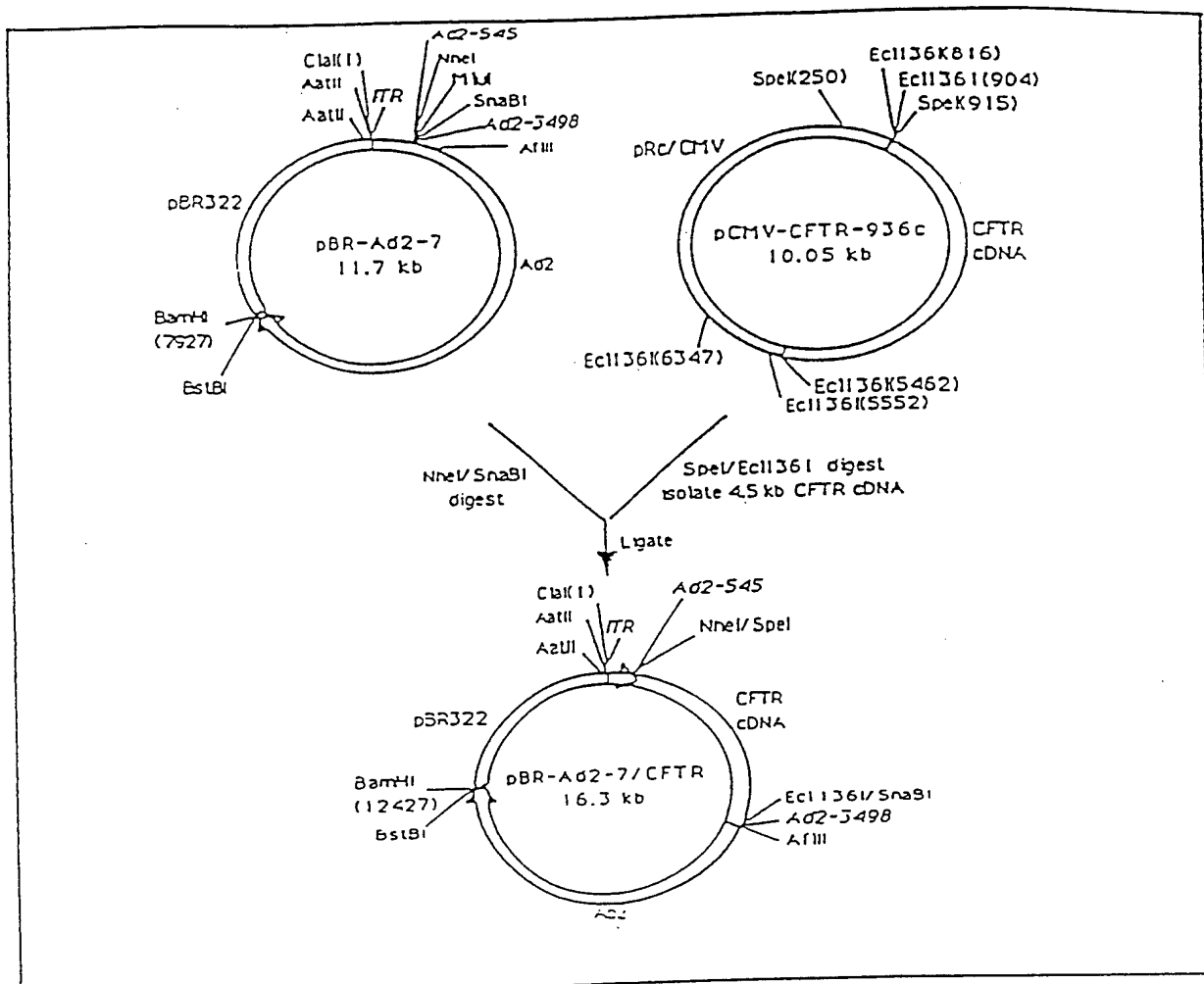


Figure 15

17/50

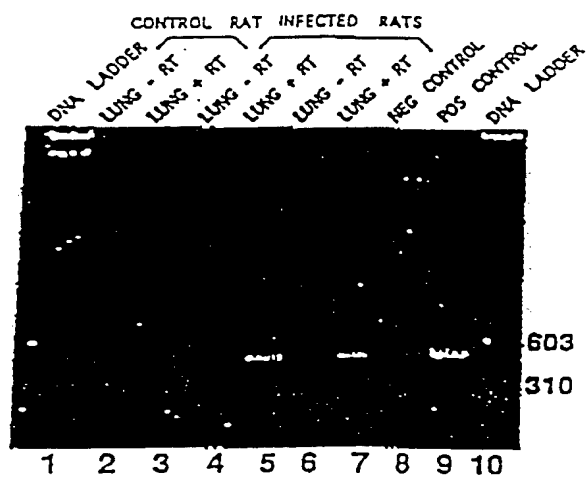


Figure 16

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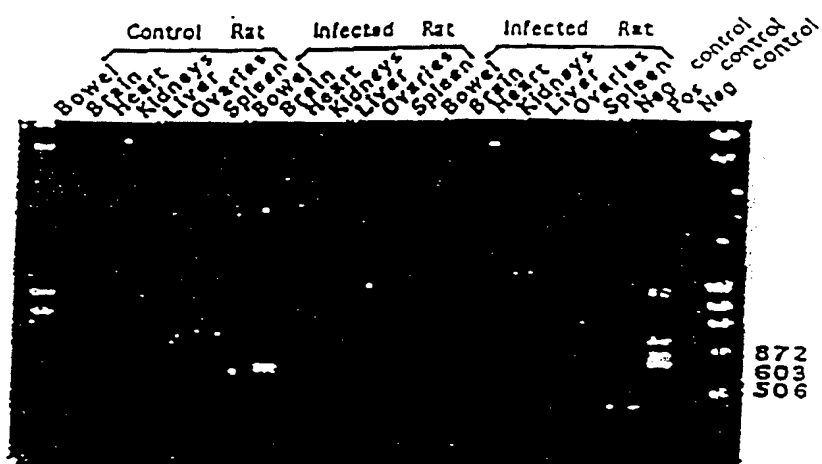


Figure 17

19/50

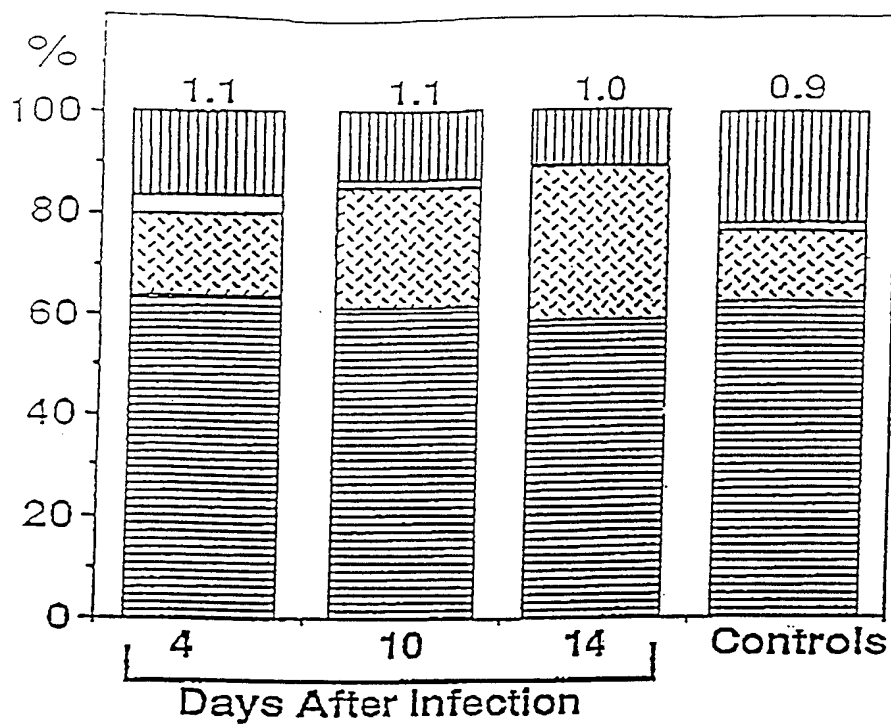


Figure 18A

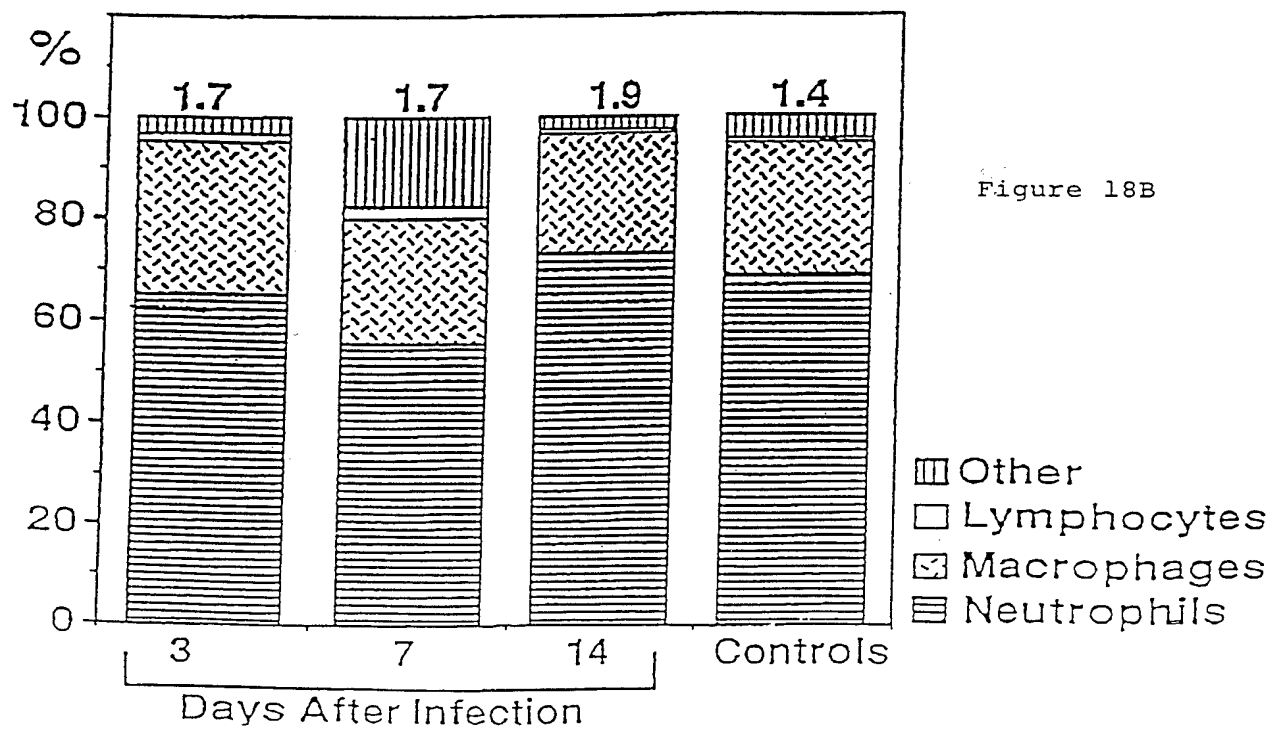


Figure 18B

20/50

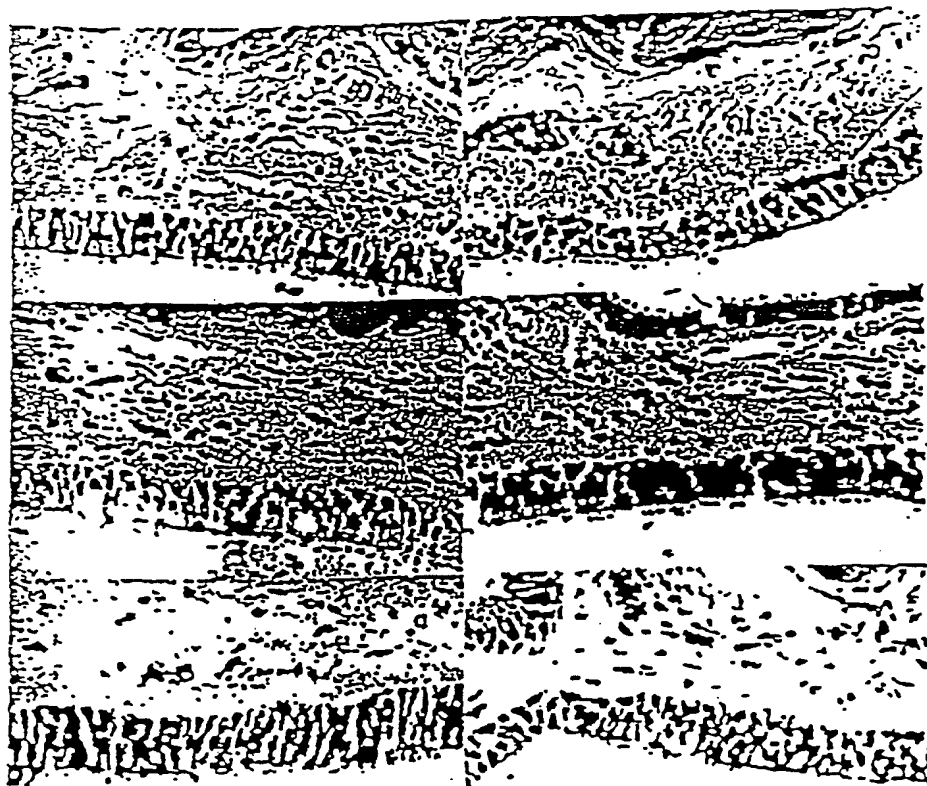


Figure 19

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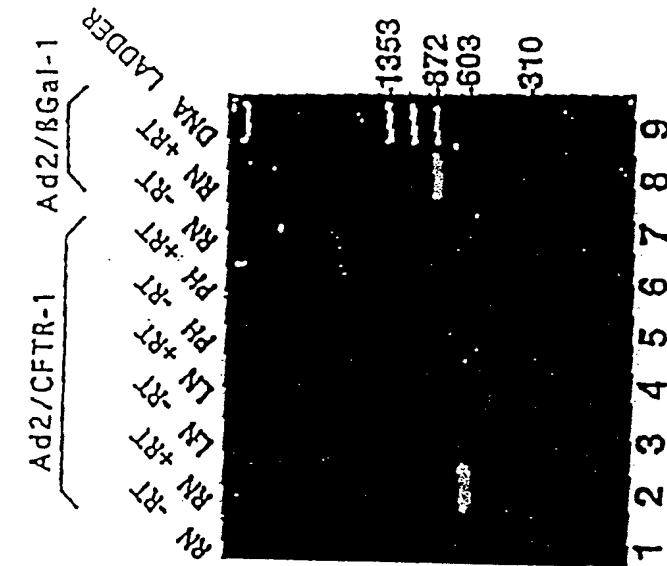


Figure 20A

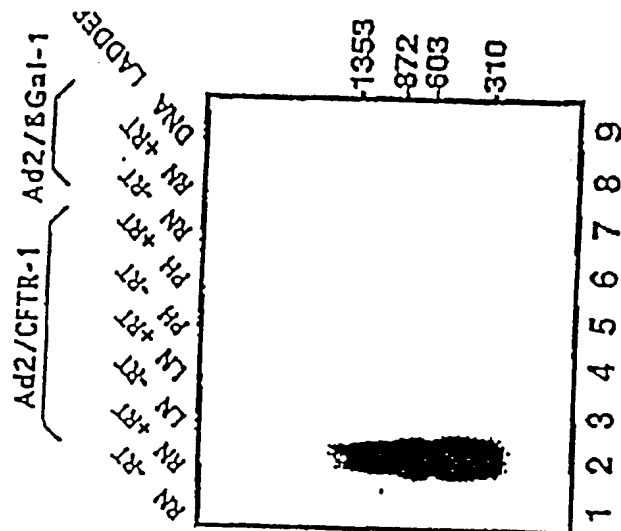


Figure 20B

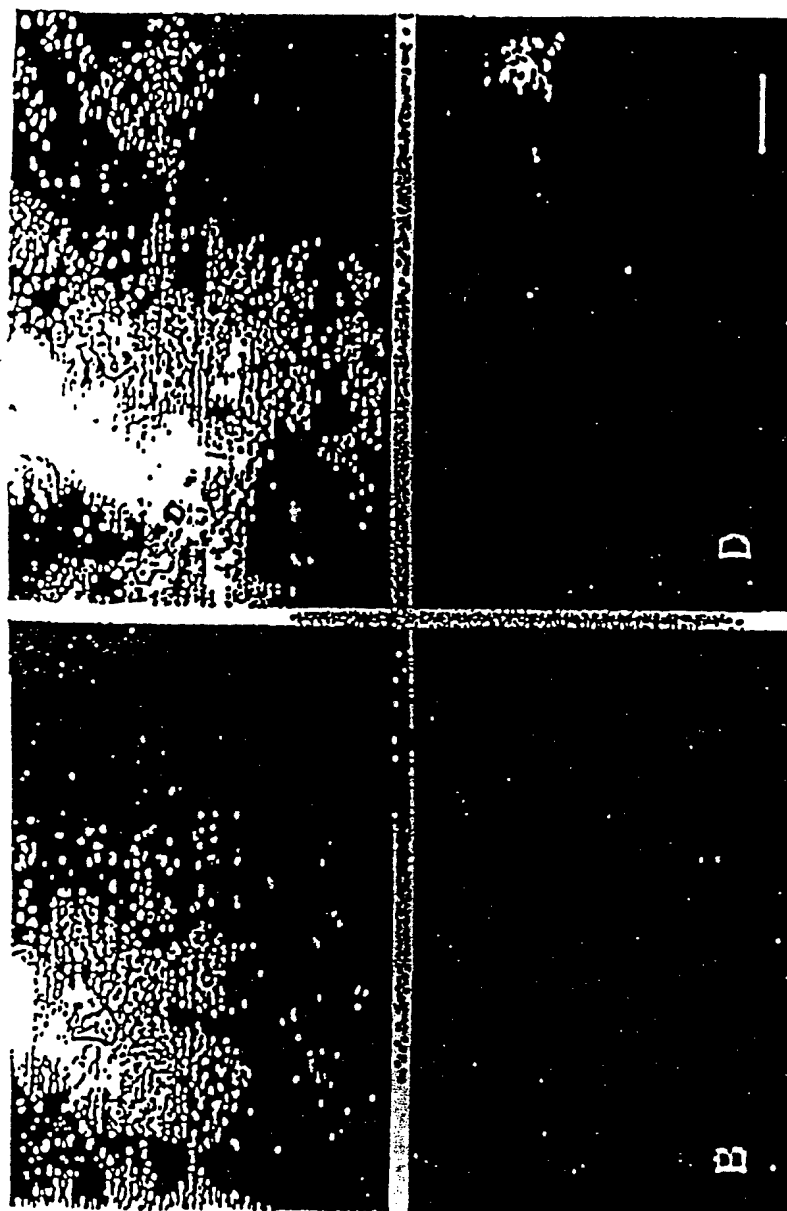


Figure 21

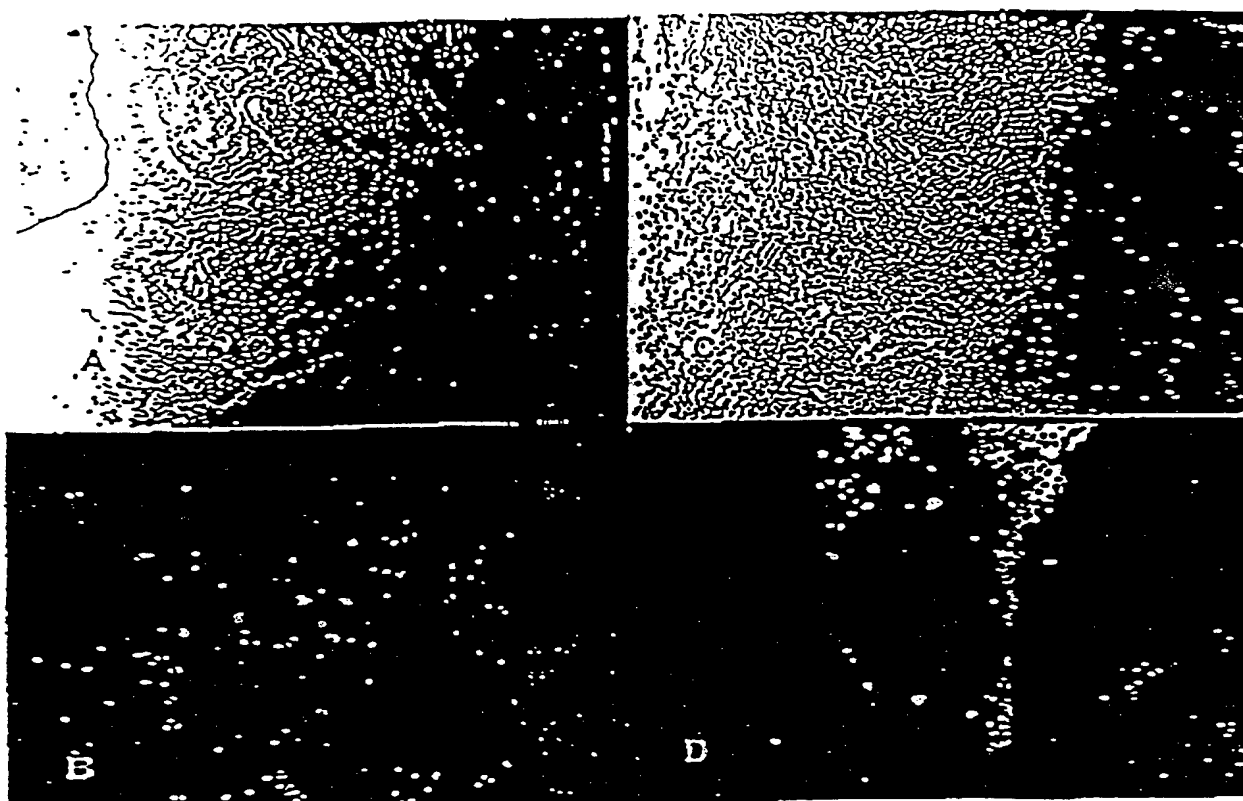
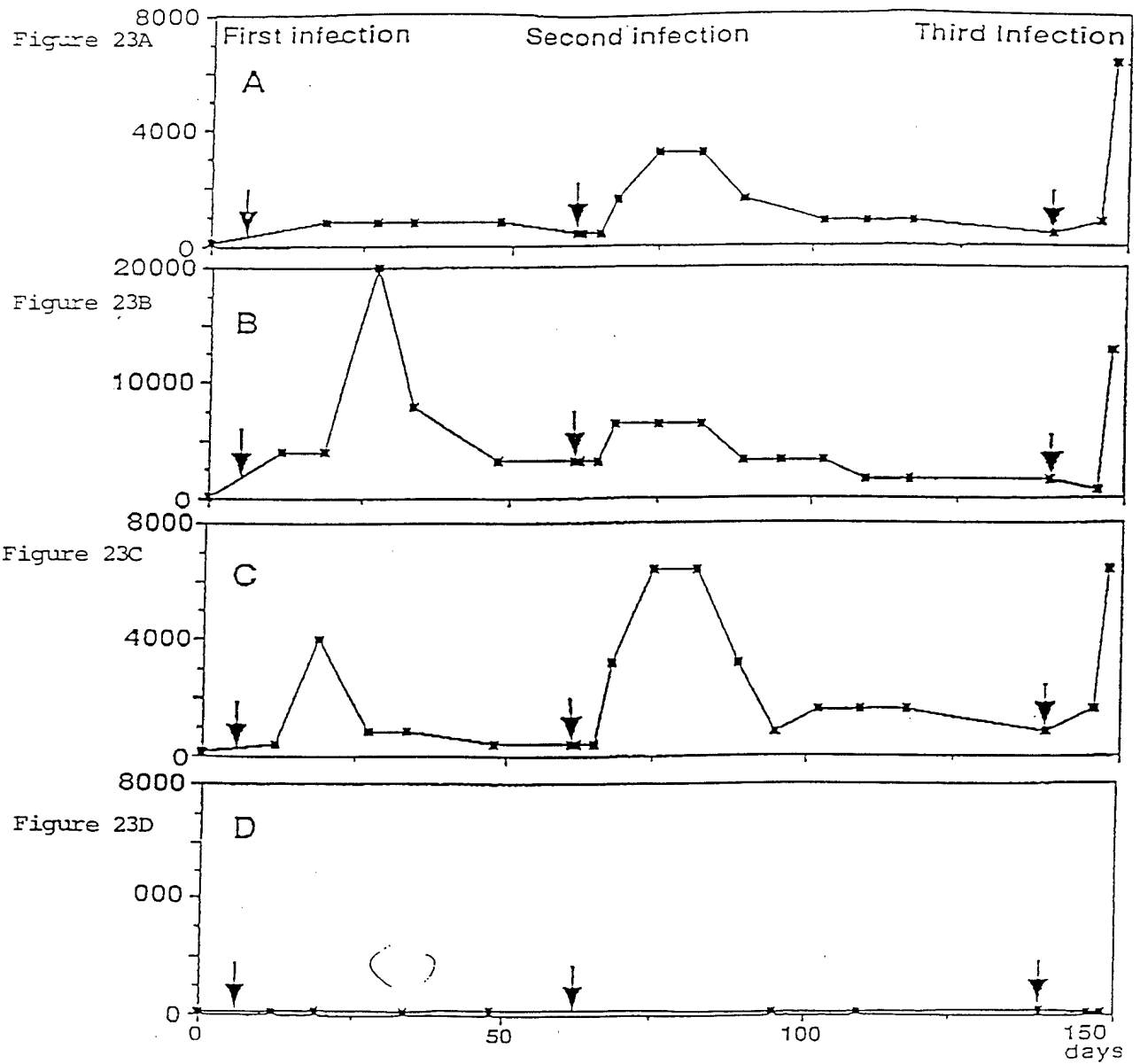


Figure 22

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ANTIBODY TITERS



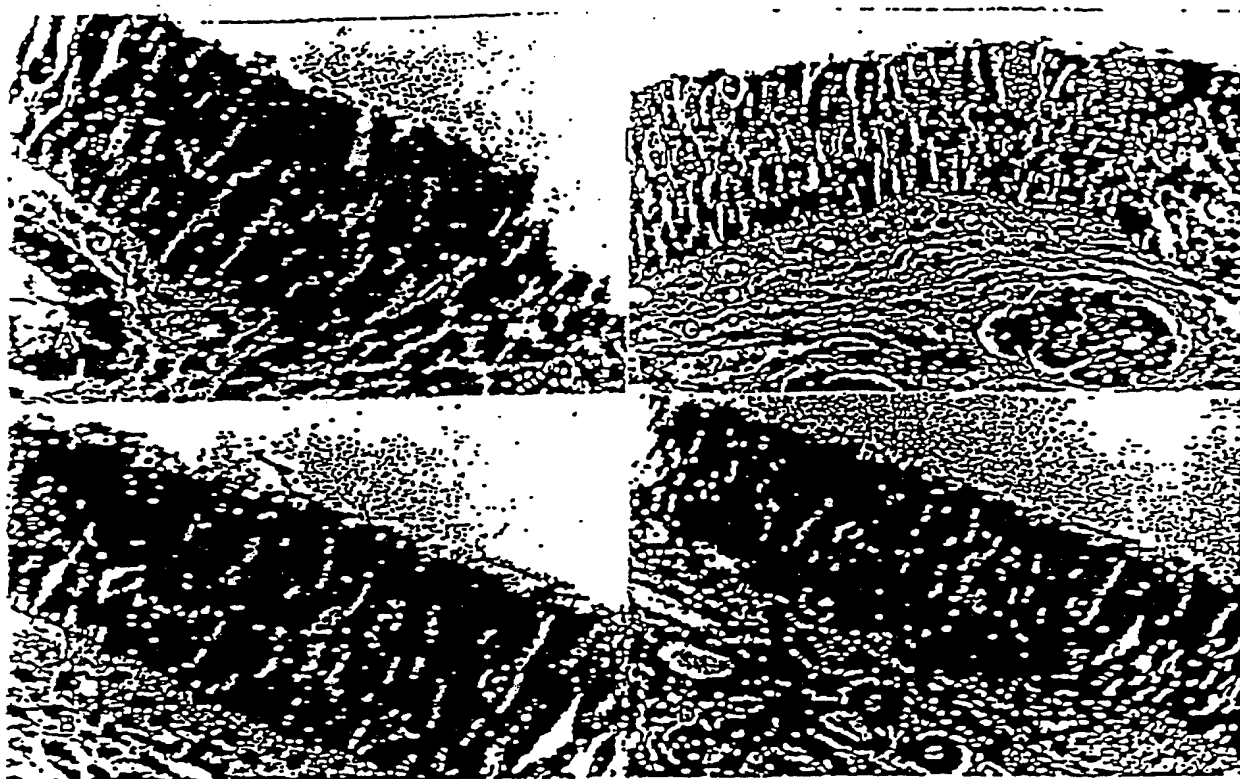


Figure 24

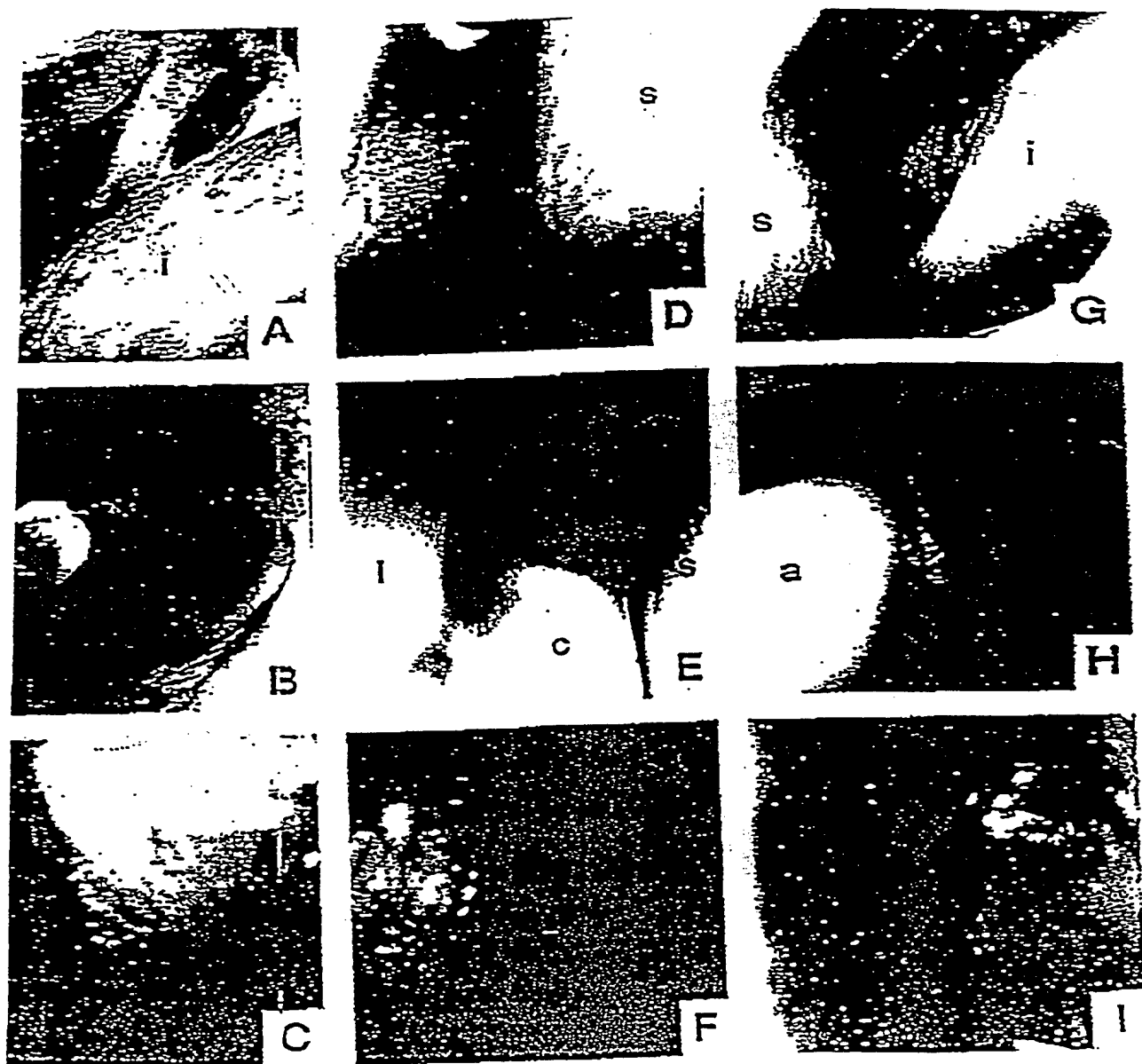


Figure 25



Figure 26

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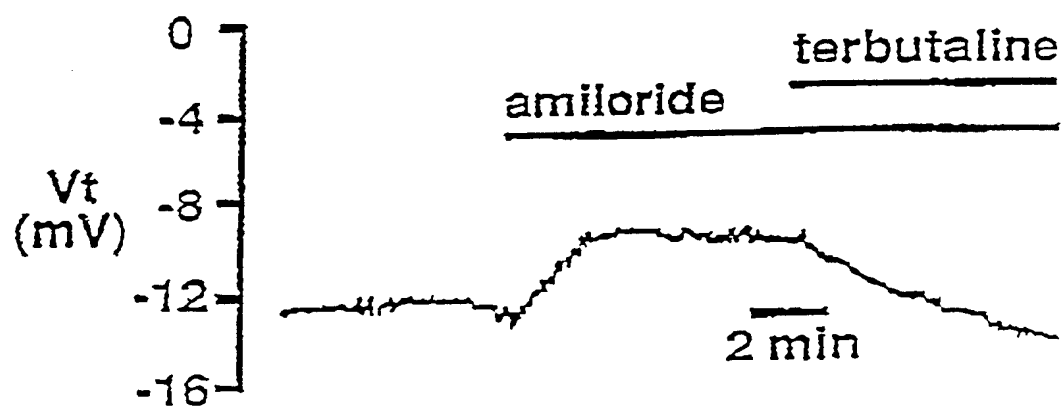


Figure 27

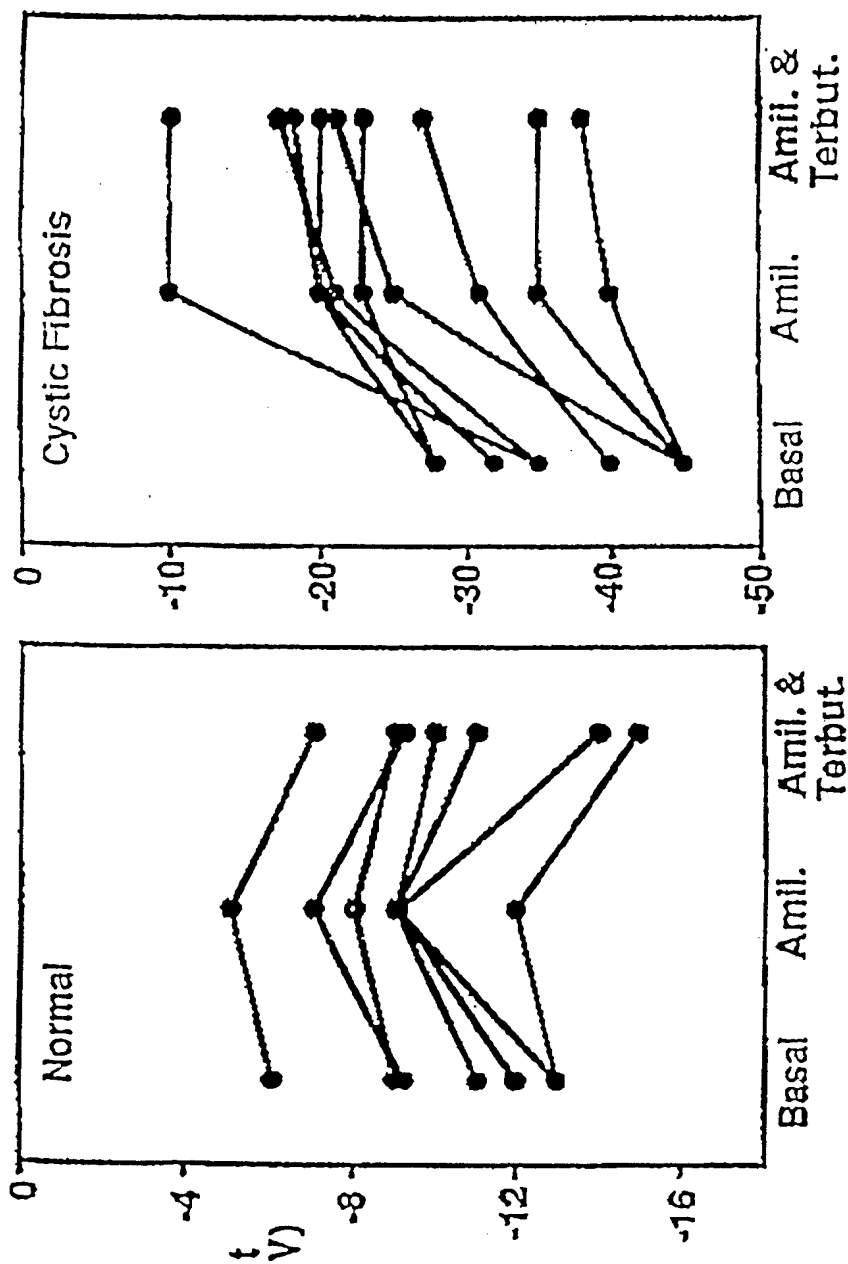


Figure 28B

Figure 28A

30/50

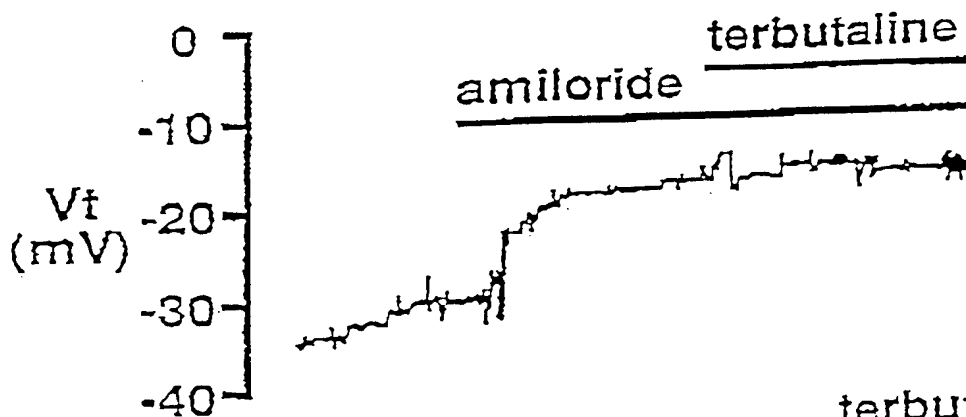


Figure 29A

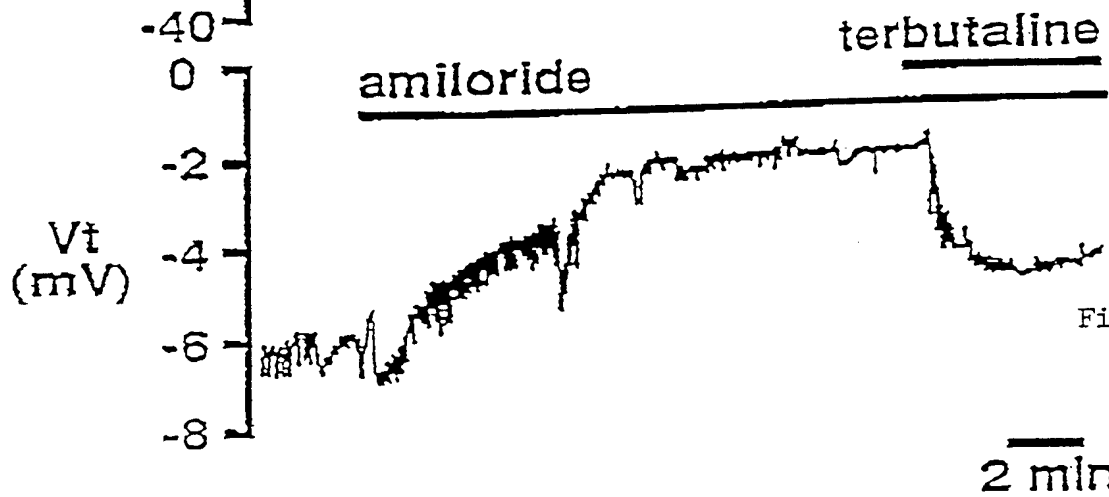


Figure 29B

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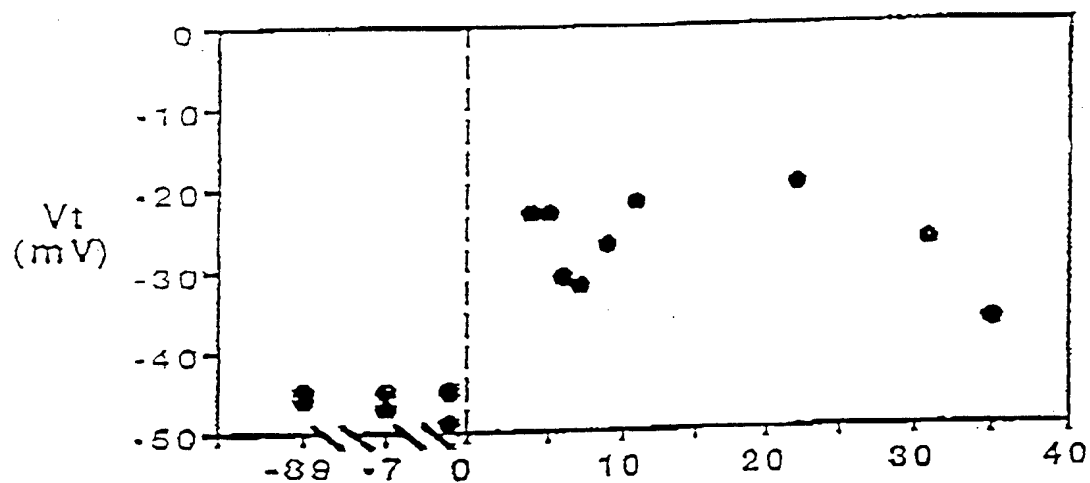


Figure 30A

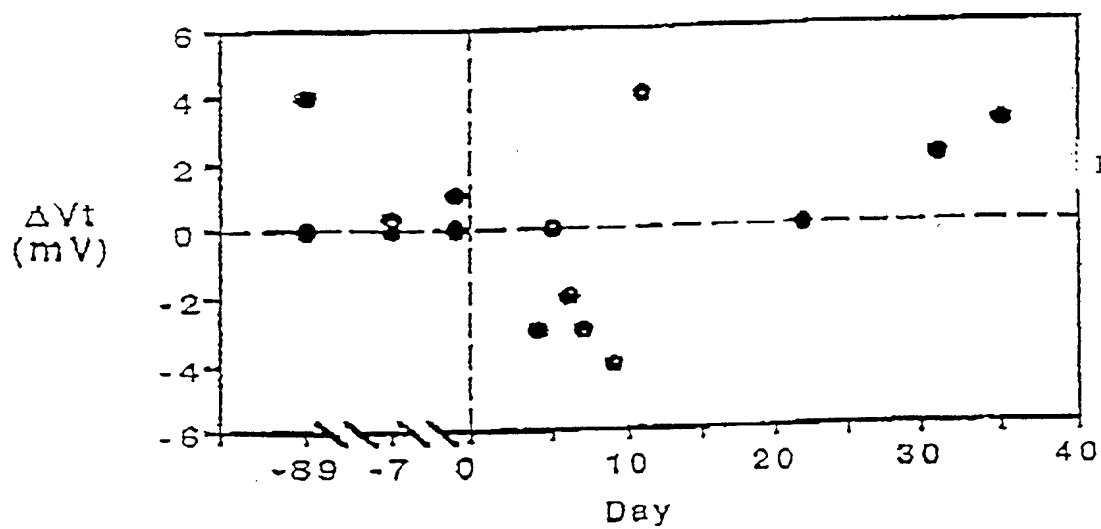


Figure 30B

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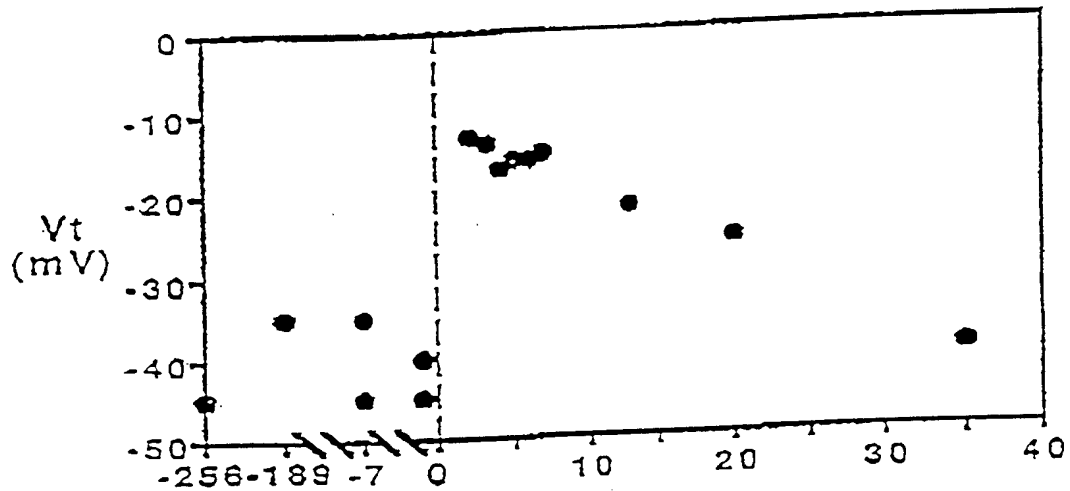


Figure 30C

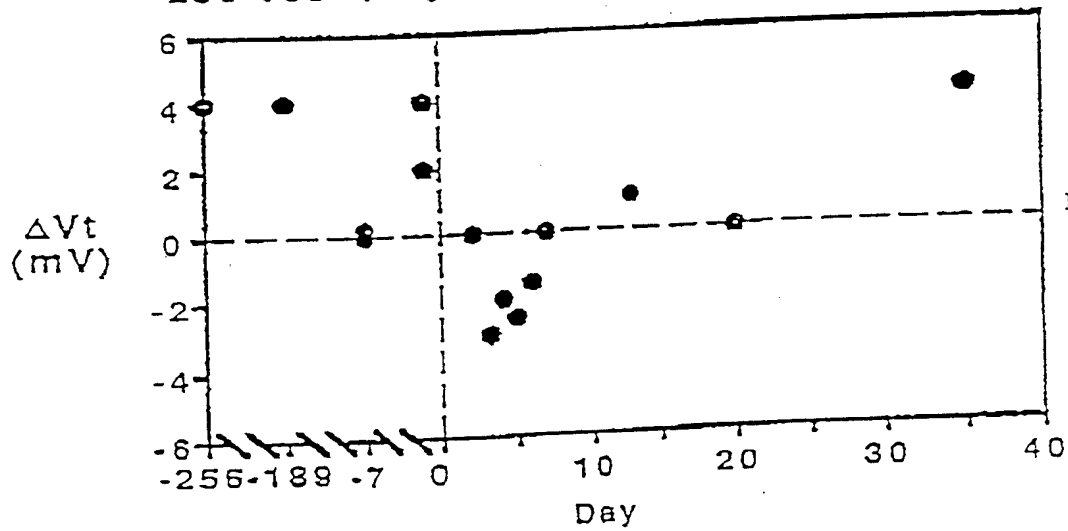
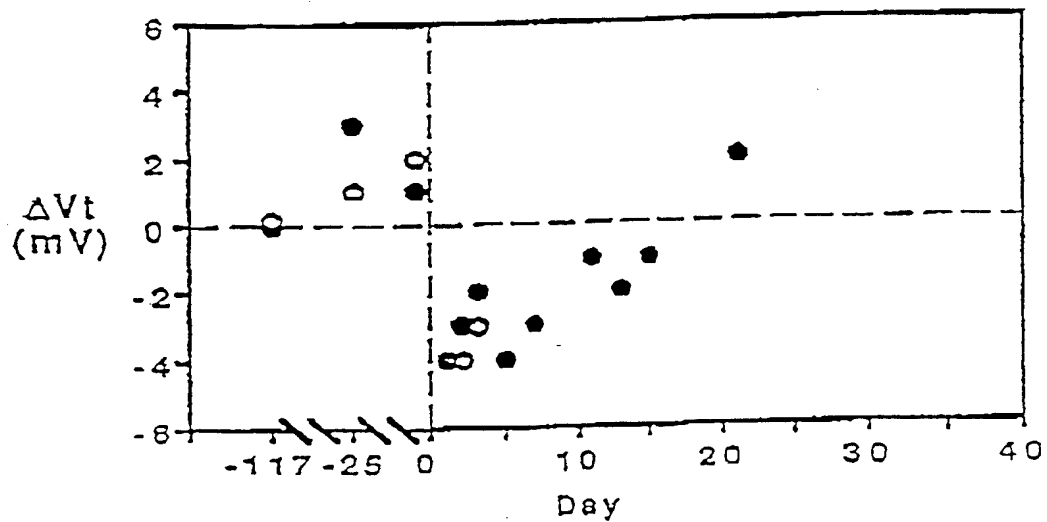
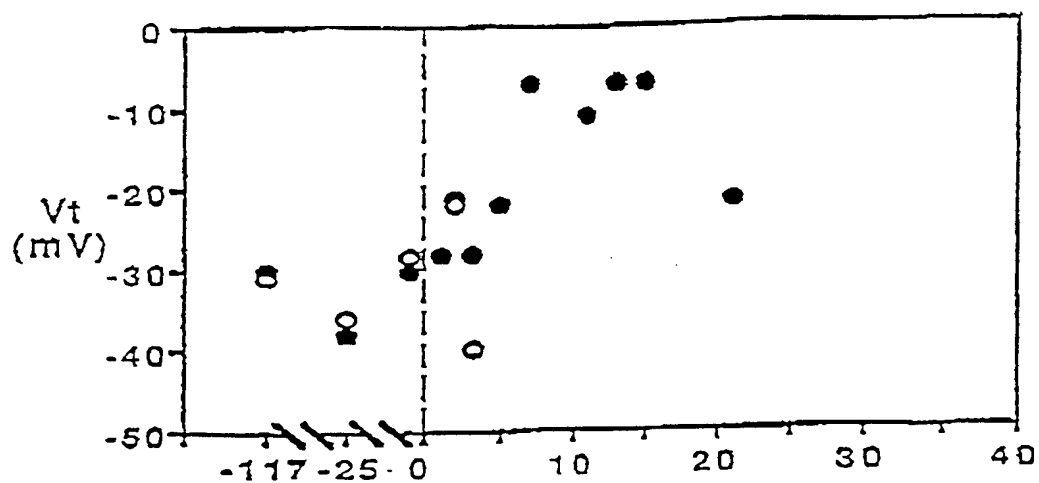


Figure 30D



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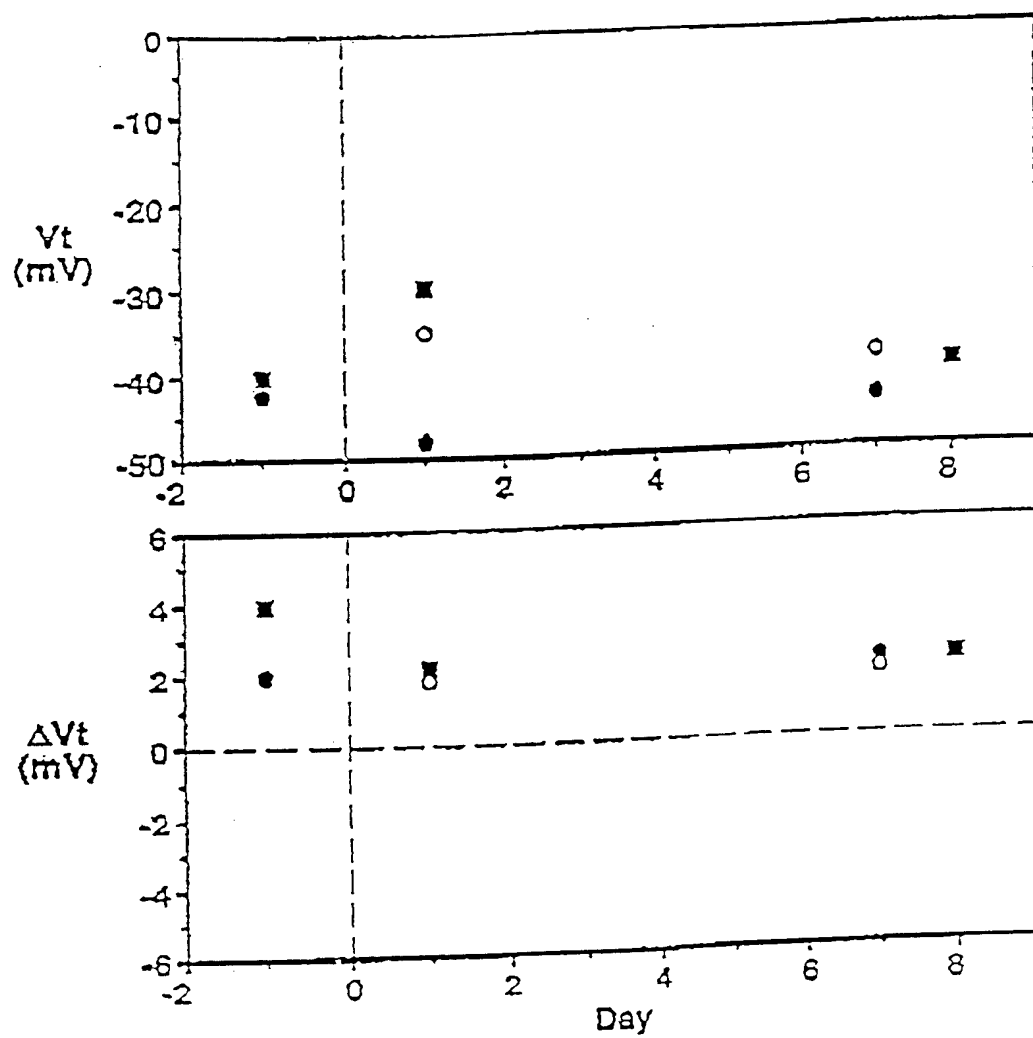
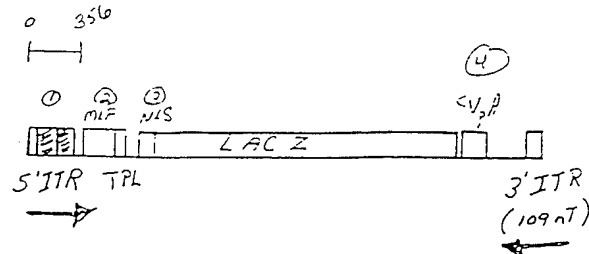
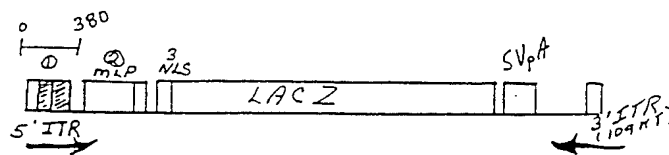


Figure 31

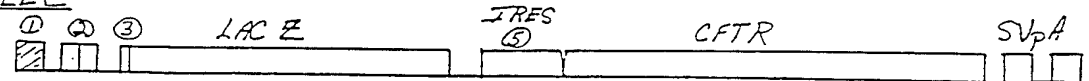
35/50



- ① Adenovirus Type 2 packaging signal and E1 enhancer Region
 ② Adenovirus Type 2 major Late Promoter and Tri-partite Leader
 ③ SV40 T-antigen nuclear Localization Signal
 ④ SV40 Poly Adenylation Signal

PAVII

- ① Adenovirus Type 2 packaging signal and E1 enhancer Region
 ② Adenovirus Type 2 major Late Promoter and Tri-partite Leader
 ③ SV40 T-antigen nuclear Localization Signal
 ④ SV40 Poly Adenylation Signal

PAV I/II LEC

- ⑤ EMC VIRUS Internal Ribosomal entry site - for Polycistronic Translation

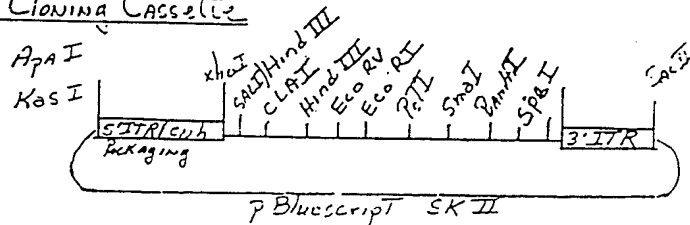
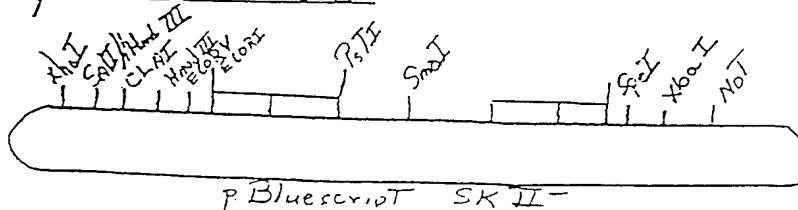
PAVI Cloning CassetteExpression Cassette

Figure 32

36/50

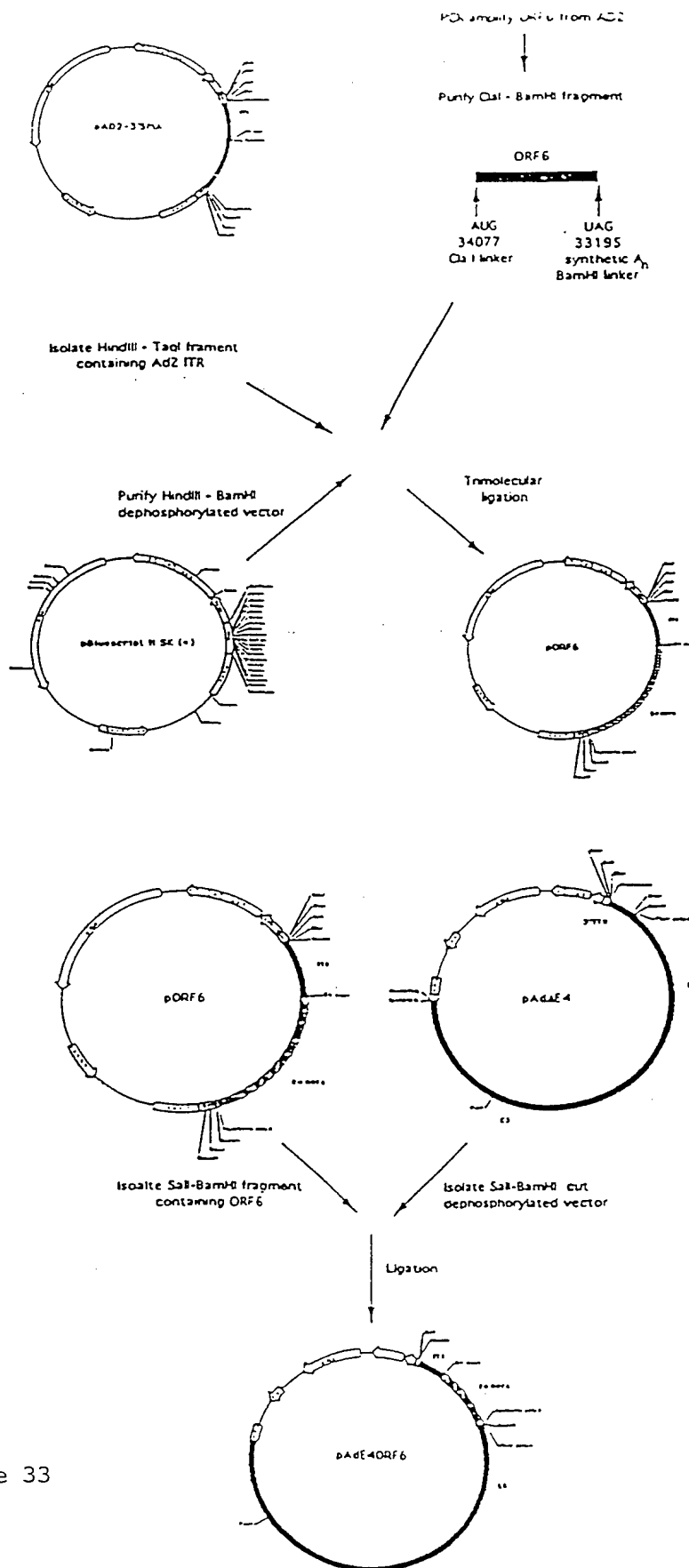


Figure 33

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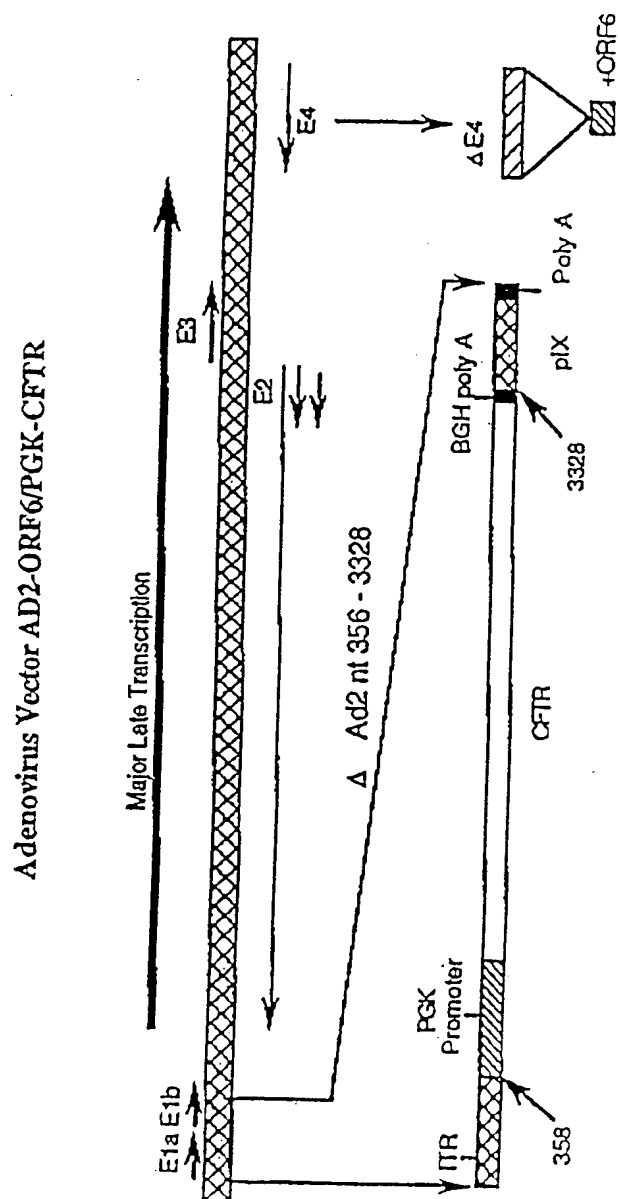


Figure 34

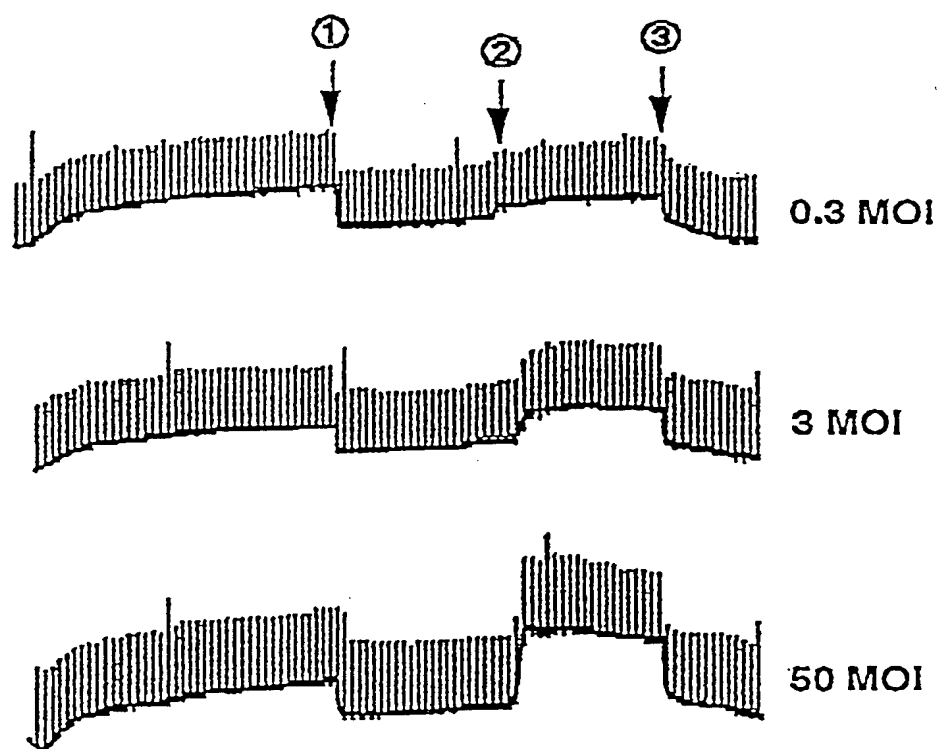


Figure 35

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Figure 36C



Figure 36D

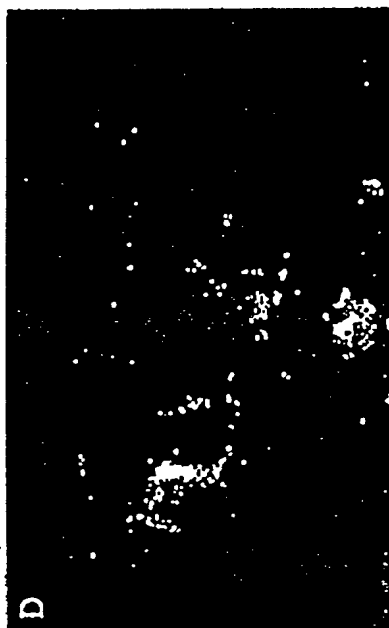
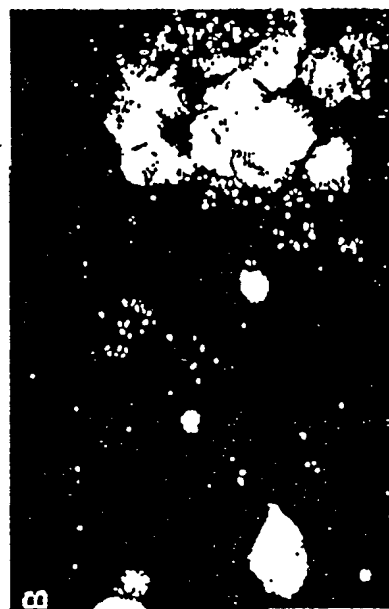


Figure 36A



Figure 36B



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Figure 37C

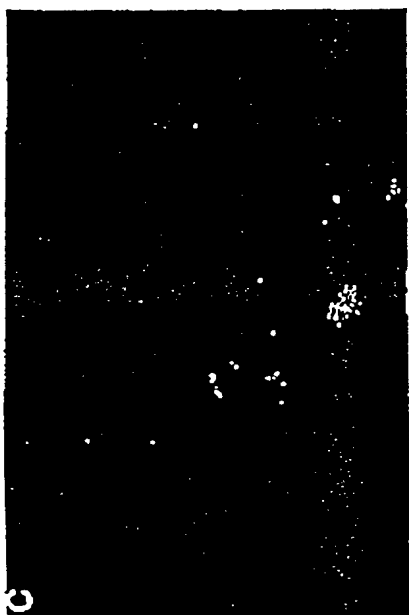


Figure 37D



Figure 37A

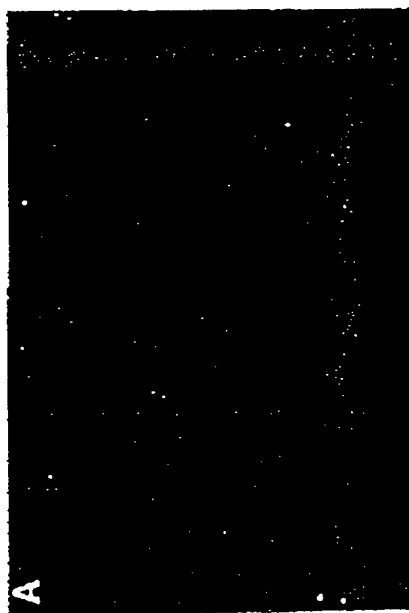
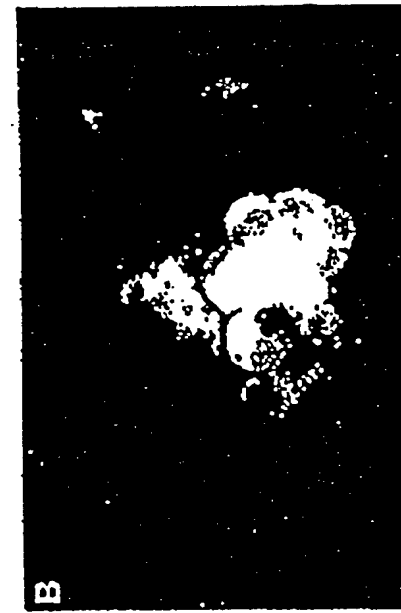


Figure 37B



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Figure 38C



Figure 38D



Figure 38A

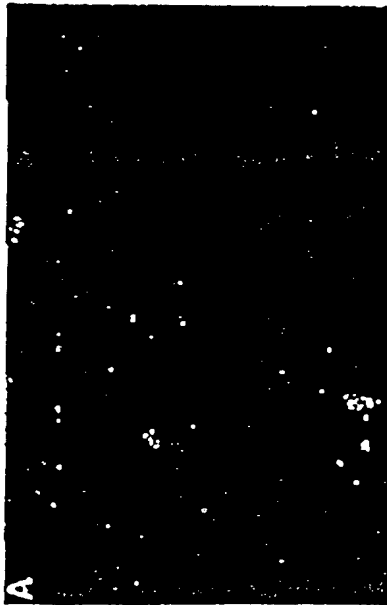
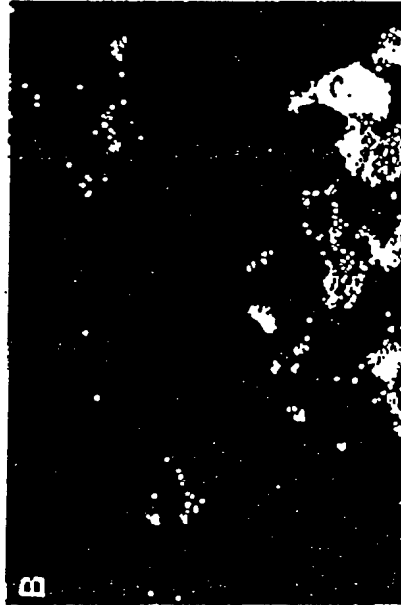


Figure 38B



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CLINICAL SIGNS MONKEY C					AGE 7 YEARS
DATE	EXAMINATION	HEART RATE	RESP RATE	TEMPERATURE	WEIGHT
		(beats/min)	(breath/min)	(Celsius)	(Kg)
5/11/93	NORMAL	112	16	37.8	6.4
5/11/93	INFECTION				
5/14/93	NORMAL	98	14	38.1	
5/18/93	NORMAL	104	16	38.3	
6/4/93	NORMAL	108	16	38.2	
6/18/93	NORMAL	112	16	38.4	
6/24/93	NORMAL	116	18	38.8	
6/24/93	INFECTION				
16/28/93	NORMAL	104	18	37.9	
7/5/93	granulation	116	16	37.4	
7/12/93	NORMAL	114	20	38.3	
9/17/93	NORMAL	108	16	38.3	7

Figure 39A

CLINICAL SIGNS MONKEY D					AGE 7 YEARS
DATE	EXAMINATION	HEART RATE	RESP RATE	TEMPERATURE	WEIGHT
		(beats/min)	(breath/min)	(Celsius)	(Kg)
5/11/93	NORMAL	108	18	38.3	6.25
5/11/93	INFECTION				
5/14/93	NORMAL	100	20	38.4	
5/18/93	NORMAL	98	20	38.4	
6/4/93	NORMAL	106	18	37.9	
6/18/93	NORMAL	100	19	38.4	
6/24/93	NORMAL	106	16	37.8	
6/24/93	INFECTION				
16/28/93	NORMAL	104	16	37.4	
7/5/93	NORMAL	102	14	38.8	
7/12/93	granulation	114	16	38	
9/17/93	NORMAL	104	16	38.3	6.4

Figure 39B

CLINICAL SIGNS MONKEY E					AGE 11 YEARS
DATE	EXAMINATION	HEART RATE	RESP RATE	TEMPERATURE	WEIGHT
		(beats/min)	(breath/min)	(Celsius)	(Kg)
5/11/93	NORMAL	120	18	28.3	10
5/11/93	INFECTION				
5/14/93	NORMAL	112	20	37.9	
5/18/93	NORMAL	108	22	38.4	
6/4/93	NORMAL	112	20	38.3	
6/18/93	NORMAL	106	20	38.3	
6/24/93	NORMAL	108	18	38.9	
6/24/93	INFECTION				
16/28/93	NORMAL	112	20	38	
7/5/93	NORMAL	106	22	38.3	
7/12/93	NORMAL	114	16	38	
9/17/93	NORMAL	114	16	38.3	8.75

Figure 39C

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Monkey C

Clinical Lab Results From Monkey C

DATE	11-May	14-May	18-May	4-Jun	18-Jun	24-Jun	24-Jun	12-Jul	17-Sep
WBC/mm ³	6.7	9	8.9	7.1	7.9	7.3		10.6	8.1
NEUT/mm ³	1850	3990	3060	1480	3550	3450		2210	3950
LYMP/mm ³	4460	4220	4770	4780	3640	2670		7270	3770
MONO/mm ³	120	520	600	360	420	550		480	340
EOS/mm ³	30	110	190	120	80	400		250	70
HEMOG. gr/dl	12.2	12	12.6	12.8	14	13.5		13.7	13.9
HEMATOCR. %	38	38	42	41	45	39		46	43
PLAT k/mm ³	311	319	343	338	308	281		324	432
ESR	<1	1	1	1	0	<1		<1	<1
NA mEq/l	149	148	147		151	147		149	153
K mEq/l	3.6	3.6	2.6		3.6	3.1		3.4	3.6
Cl mEq/l	111	106	107		112	108		109	113
CO ₂ mEq/l	19	20	20		22	21		19	19
BUN mg/dl	11	18	11		14	13		16	23
CREAT mg/dl	1.1	1	1.2		1.1	1		1.1	1.2
GLUCOSE mg/dl	68	56	81		67	87		74	58
ALB gr/dl	4.7	4.3	4.7		4.9	4.2		4.5	4.5
T. PROT. gr/dl	7.3	6.7	7.1		7.4	6.9		7.1	7.4
CALCIUM mg/dl	10	9.3	9.9		10.2	9		10.1	9.5
PO ₄ mg/dl	3.3	5.9	5.7		2.9	5		3.7	3.4
ALK. PH IU/l	117	376	375		117	76		116	184
TOT BIL mg/dl	0.3	0.2	0.2		0.2	0.1		0.2	0.3
AST IU/l	38	37	45		28	25		45	34
LDH IU/l	601	599	740		277	408		458	220
URIC Ac mg/dl	0.1	0.1	<0.1		0.1	0.1		<0.1	0.1

Figure 40A

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Monkey D

Clinical Lab Results From Monkey D									
DATE	11-May	14-May	18-May	4-Jun	18-Jun	24-Jun	12-Jul	17-Sep	
WBC/mm ³	7						9.4	8.3	
NEUT/mm ³	2860	1980	3060	1090	6230	1740		3180	
LYMP/mm ³	3660	4180	6100	4770	1820	4750		3230	
MONO/mm ³	160	410	340	500	500	190		670	
EOS/mm ³	50	150	210	110	240	130		210	
HEMOG. gr/dl	10.9	13.7	14.7	13.6	13.9	13.6		14.5	
HEMATOCR.%	35	42	49	44	43	43	44	47	
PLAT k/mm ³	268	277	413	369	265	300	284	348	
ESR	1	2	<1	1	0	<1	<1	<1	
NA mEq/l	147	150	150		149	147	148	148	
K mEq/l	3.5	3.5	3.6		3.5	3.4	3.5	3	
Cl mEq/l	109	106	110		111	108	109	109	
CO ₂ mEq/l	19	20	20		23	20	19	16	
BUN mg/dl	19	18	20		10	16	18	12	
CREAT mg/dl	1.1	1	1.1		1.1	1	1	1	
GLUCOSE mg/dl	65	81	72		92	78	66	88	
ALB gr/dl	4.3	4.7	5.2		4.2	4.6	4.5	4.7	
T. PROT, gr/dl	6.6	7.4	7.8		6.8	6.8	7.1	7.6	
CALCU. mEq/dl	9.3	10.1	10.4		9.6	9	10.3	9.5	
PO ₄ mg/dl	6.2	3.5	3.6		2.8	5	5.6	4.7	
ALK. PH IU/l	426	104	116		82	337	328	101	
TOT BIL mg/dl	0.1	0.3	0.2		0.2	0.1	0.1	0.2	
AST IU/l	29	32	103		55	27	25	21	
LDH IU/l	520	496	912		768	615	252	227	
URIC Ac mg/dl	0.1	<0.1	<0.1		0.1	0.1	<0.1	0.1	

Figure 40B

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Monkey E

Clinical Lab Results From Monkey E

DATE	11-May	14-May	18-May	4-Jun	18-Jun	24-Jun	12-Jul	17-Sep
WBC/mm ³	8.7			5.3	8.8	8.6	6.9	8.1
NEUT/mm ³	4850			3210	4480	2040		2592
LYMP/mm ³	3060			1510	3360	5610		5265
MONO/mm ³	120			280	350	460		162
EOS/mm ³	30			150	80	170		81
HEMOG. gr/dl	12.9			13.7	12.6	12.4	13.8	13.9
HEMATOCR. %	40			42	41	38	44	43
PLAT k/mm ³	291			287	291	300	269	432
ESR	1			1	0	<1	<1	<1
NA mEq/l	148		147		148	149	148	150
K mEq/l	3		2.6		3.7	3.6	3.1	3.8
Cl mEq/l	110		107		110	111	109	110
CO ₂ mEq/l	16		20		22	23	21	20
BUN mg/dl	8		11		15	13	14	17
CREAT mg/dl	1.1		1.2		1.1	1	1	1.2
GLUCOSE mg/dl	115		102		86	65	87	69
ALB gr/dl	4		4.4		4.5	4.8	4	4.5
T. PROT. gr/dl	6.7		7.1		7	7.3	6.8	7
CALCIUM mg/dl	9.3		9.4		9.8	9.7	9.7	9.4
PO ₄ mg/dl	3.5		4.2		5.1	3.3	4.6	4.1
ALK. PH IU/l	68		90		393	116	75	355
TOT BIL. mg/dl	0.2		0.3		0.1	0.2	0.2	2
AST IU/l	32		47		27	28	28	24
LDH IU/l	416		571		277	481	247	200
URIC Ac mg/dl	0.1		<0.1		0.1	0.1	<0.1	<0.1

S E C O N D I N F E C T I O N

F I R S T I N F E C T I O N

Figure 40C

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CYTOLOGY MONKEY C

DATE	5/11/93	5/18/93	6/4/93	6/18/93	6/24/93	6/24/93	8/28/93	9/17/93
LEFT NOSTRIL								
Sq. Epith.	88	78	63	72	74	S	B	89
Resp. Epith.	30	18	34	24	25	E	I	30
Neutrophils	1	2	3	2	0	C	O	0
Lymphocytes	1	2	0	1	1	O	P	0
Eosinophils	0	0	0	1	0	N	S	1
						D	Y	

CYTOLOGY MONKEY D

DATE	5/11/93	5/18/93	6/4/93	6/18/93	6/24/93	6/24/93	7/5/93	9/17/93
LEFT NOSTRIL								
Sq. Epith.	60	60	72	72	84	S	B	73
Resp. Epith.	39	39	26	25	14	E	I	25
Neutrophils	1	1	0	1	2	C	O	2
Lymphocytes	0	2	2	1	0	O	P	0
Eosinophils	0	0	0	1	0	N	S	0
						D	Y	

CYTOLOGY MONKEY E

DATE	5/11/93	5/18/93	6/4/93	6/18/93	6/24/93	6/24/93	7/12/93	9/17/93
LEFT NOSTRIL								
Sq. Epith.	60	60	72	72	84	S	B	73
Resp. Epith.	39	39	26	25	14	E	I	25
Neutrophils	1	1	0	1	2	C	O	2
Lymphocytes	0	2	2	1	0	O	P	0
Eosinophils	0	0	0	1	0	N	S	0
						D	Y	

Figure 41

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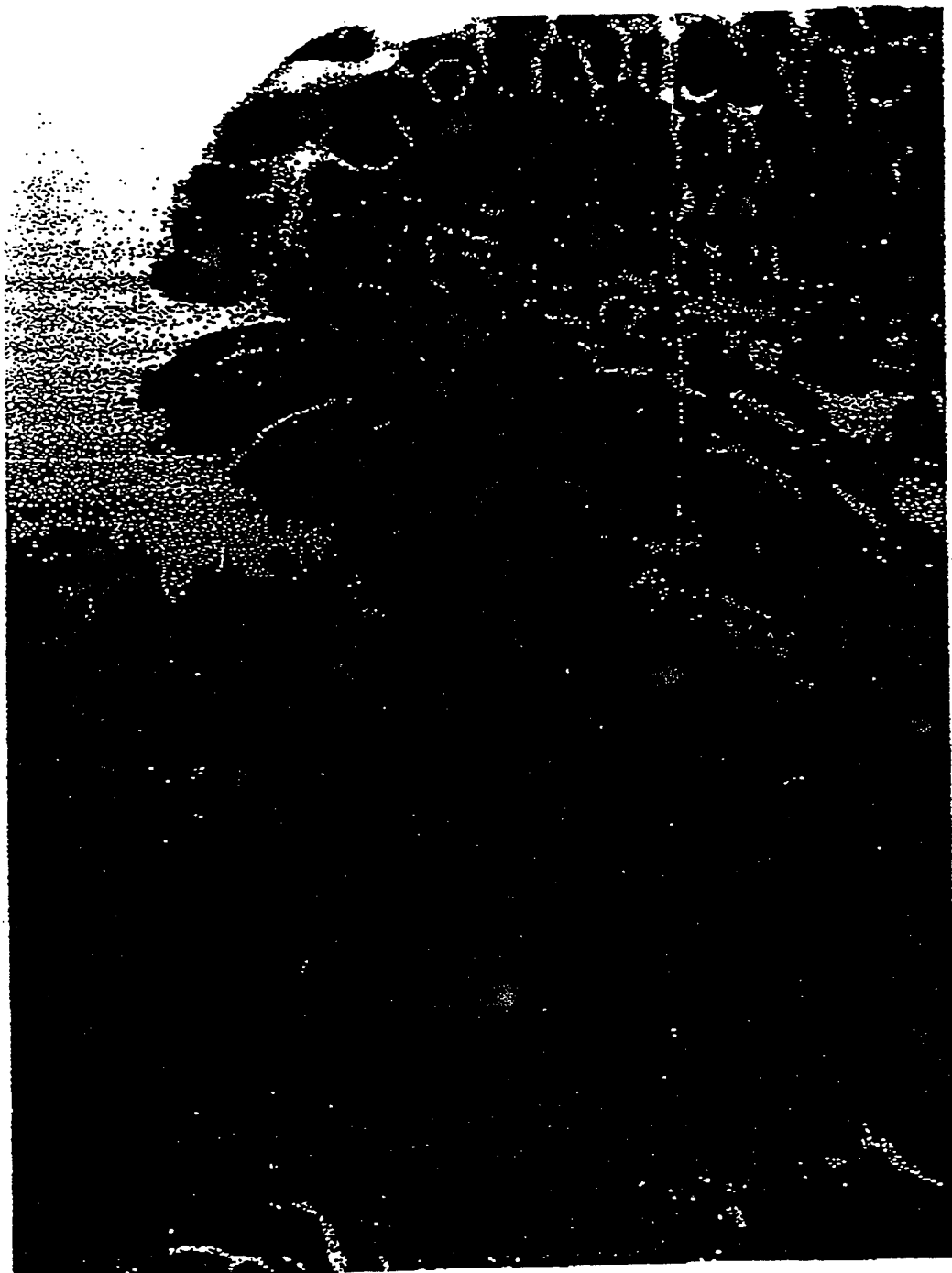


Figure 42

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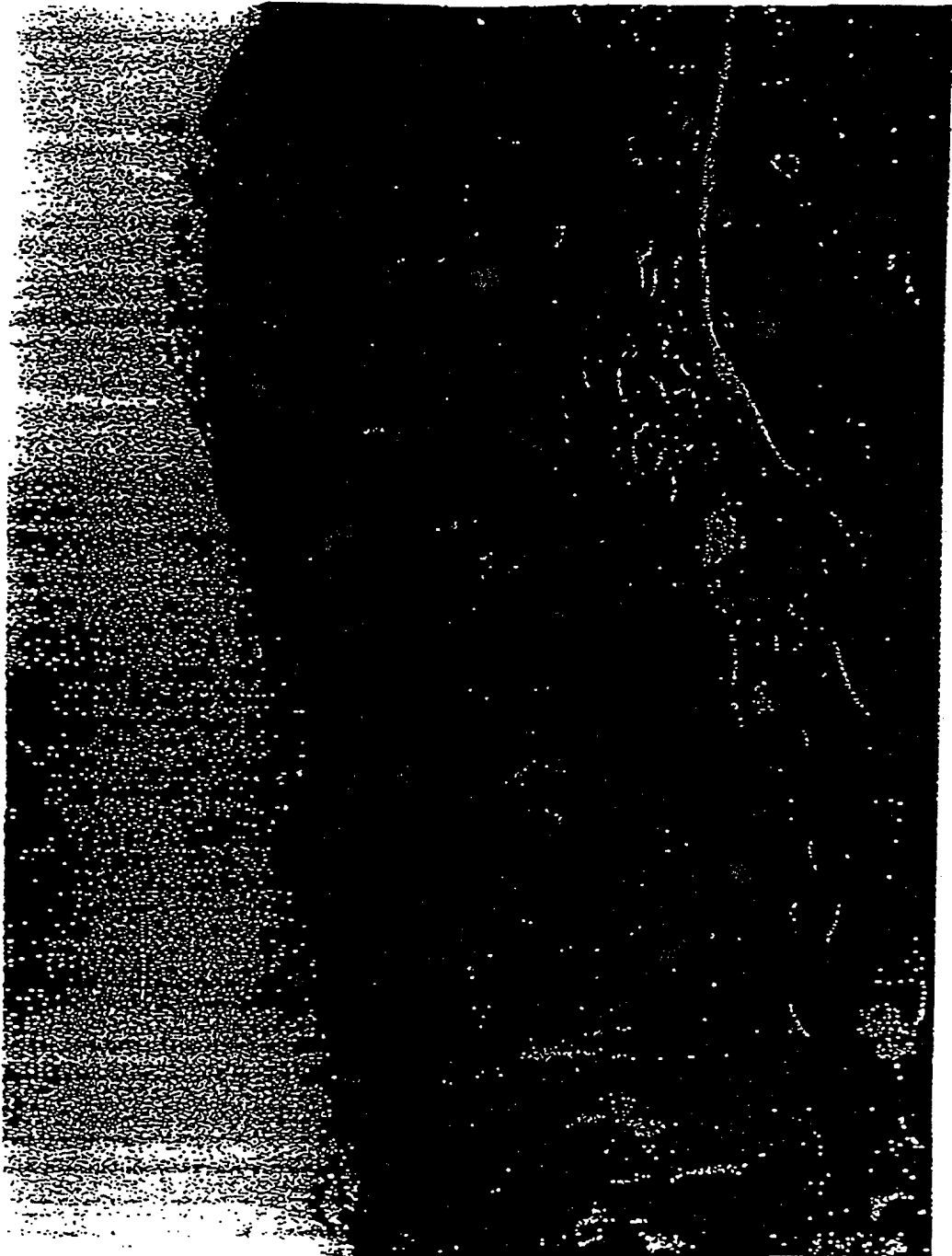


Figure 43



Figure 44

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NEUTRALIZING ANTIBODIES •

